

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 27, 2005, 20:29:56 ; Search time 230 Seconds  
(without alignments)  
1128.845 Million cell updates/sec

Title: US-10-768-886-2  
Perfect score: 1953  
Sequence: 1 MDGAPVAEFPRTWTHGGRYL.....DQMKQLIFNEATEMPNIRY 368

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1942.5	99.5	369	2	Q7FNE2_ORYSA
2	1942.5	99.5	369	2	Q9FQM3_ORYSA
3	1938.5	99.3	369	2	Q9AXF2_ORYSA
4	1927.5	98.7	369	2	Q9FSE6_ORYSA
5	1878.5	96.2	357	2	Q8GZ23_ORYSA
6	1837	94.1	370	2	Q4QWQ7_SACOP
7	1819.5	93.2	369	2	Q43379_AVEA
8	1812.5	92.8	369	2	Q81599_WHEAT
9	1774	90.8	406	2	Q9ZMJ6_MAIZE
10	1519.5	77.8	371	2	Q5K604_SOYBN
11	1505.5	77.1	371	2	Q9M6S1_PEA
12	1504.5	77.0	371	2	Q24077_MEDSA
13	1481.5	75.9	375	2	Q8W406_TOBAC
14	1480.5	75.8	370	2	Q51V18_BRANA
15	1477.5	75.7	373	2	Q84M14_LYCES
16	1476.5	75.6	376	2	Q8H0B4_NICBE
17	1472.5	75.4	370	1	MPK3_ARATH
18	1472.5	75.4	375	2	Q40598_TOBAC
19	1464.5	75.0	369	2	Q5PZV2_9BRAS
20	1461.5	74.8	375	2	Q9LKK2_CAPAN
21	1453.5	74.4	396	2	Q7Y1Y6_LYCERS
22	1453	74.4	407	2	Q4JKX8_9CARY
23	1452.5	74.4	396	2	Q84M16_LYCES
24	1448.5	74.2	396	2	Q8LTI8_SOLTU
25	1448	74.1	387	1	MMK1_MEDSA
26	1445.5	74.0	393	1	NTF4_TOBAC
27	1445	74.0	389	2	Q9M534_EUPHIB
28	1442.5	73.9	391	2	Q5K6N6_SOYBN
29	1442	73.8	395	1	MPK6_ARATH
30	1441.5	73.8	371	2	Q04694_PETCR
31	1441.5	73.8	394	2	Q84M15_LYCERS

32	1438.5	73.7	393	2	Q04362_TOBAC	Q04362 nicotiana t
33	1438	73.6	403	2	Q683Y6_9MAGN	Q683Y6 papaver rho
34	1437.5	73.6	394	2	Q8LTI7_SOLTU	Q8LTI7 solanum tub
35	1437	73.6	394	1	MAPK_PEA	Q06060 pisum sativ
36	1436.5	73.6	393	2	Q8H0B3_NICBE	Q8H0B3 nicotiana b
37	1432.5	73.3	398	2	Q84U15_ORYSA	Q84U15 oryza sativ
38	1430	73.2	365	2	Q9XGY8_IPOBA	Q9XGY8 ipomoea bat
39	1426	73.0	387	2	Q84XZ7_PETCR	Q84XZ7 petroselinu
40	1421.5	72.8	370	2	Q84XZ5_PETCR	Q84XZ5 petroselinu
41	1421.5	72.8	394	2	Q9LKK21_CAPAN	Q9LKK21 capsicum an
42	1415	72.5	403	2	Q84XZ3_WHEAT	Q84XZ3 triticum ae
43	1396.5	71.5	399	2	Q9ZMJ5_MAIZE	Q9ZMJ5 zea mays (m
44	1334.5	68.3	265	2	Q8S3T6_ORYSA	Q8S3T6 oryza sativ
45	1334.5	68.3	392	2	Q6ZD93_ORYSA	Q6ZD93 oryza sativ

ALIGNMENTS

RESULT 1

Q7FNE2\_ORYSA PRELIMINARY; PRT; 369 AA.  
AC Q7FNE2;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE MAP Kinase.  
GN Name=msrmk2;  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzaeae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=leaf;  
RX MEDLINE=22069893; PubMed=12074577; DOI=10.1016/S0006-291X(02)00571-5;  
RA Agrawal G.K., Kakwal R., Iwahashi H.;  
RT "Isolation of novel rice (Oryza sativa L.) multiple stress responsive  
MAP kinase gene, OsMSRMK2, whose mRNA accumulates rapidly in response  
to environmental cues.";  
RL Biochem. Biophys. Res. Commun. 294:1009-1016(2002).  
DR EMBL; AJ486975; CAD31224.1; -; mRNA.  
DR HSSP; P24941; IB38.  
DR Gramene; Q7FNE2; -.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004707; F:MAP kinase activity; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
DR GO; GO:0004668; F:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR008351; JNK MAPK.  
DR InterPro; IPR00719; Prot\_kinase.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR InterPro; IPR001245; Tyr\_pkinase.  
DR Pfam; PF00069; Pkinase; 1.  
DR PRINTS; PR01772; JNKMAPKINASE.  
DR ProDom; PD000001; Prot\_kinase; 2.  
DR SMART; SM00220; S\_TKc; 1.  
DR SMART; SM00219; TyKc; 1.  
DR PROSITE; PS01351; MAPK; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
DR KINASE.  
SQ SEQUENCE 369 AA; 42995 MW; 417D81732635P2D3 CRC64;

Query Match 99.5%; Score 1942.5; DB 2; Length 369;  
Best Local Similarity 99.7%; Pred. No. 2.9e-113;  
Matches 368; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MDGAPVAEFPRTWTHGGRYLIDYFGNKFVTKYQPPIMPGRGAYGVCSVMNFETRE 60

Db 1 MDGAPVAFRPTMTHTGGRYLLYDIFGNKFEVNTKYQPPIMPIGRGAYGIVCSVMNFETRE 60  
QY 61 MVAIKKIANAFNMDAKRTLRKILRLHLDHENIIGIRDVIPPPIPOAFNDVYIATELM 120  
Db 61 MVAIKKIANAFNMDAKRTLRKILRLHLDHENIIGIRDVIPPPIPOAFNDVYIATELM 120  
QY 121 DTDLHHIIRSNOELSEHCQYFLYQILRGLKYIHSANVIHRDLKPSNLLNANCDLKICD 180  
Db 121 DTDLHHIIRSNOELSEHCQYFLYQILRGLKYIHSANVIHRDLKPSNLLNANCDLKICD 180  
QY 181 FGLARPSSESMDMTYVTVTRWYRAPELLNSTDYSAA-DVMSVGCIFMELINRQPLFPGR 239  
Db 181 FGLARPSSESMDMTYVTVTRWYRAPELLNSTDYSAAIDVMSVGCIFMELINRQPLFPGR 240  
QY 240 DHMHQRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIE 299  
Db 241 DHMHQRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIE 300  
QY 300 RMLTFNPLQRIITVEEALDHPYLERLHDIADEPICLEPFSFDFEQKALNEDQMKQLIFNEA 359  
Db 301 RMLTFNPLQRIITVEEALDHPYLERLHDIADEPICLEPFSFDFEQKALNEDQMKQLIFNEA 360  
QY 360 IEMNPNIRY 368  
Db 361 IEMNPNIRY 369

RESULT 2  
Q9FQM3\_ORYSA  
ID Q9FQM3\_ORYSA PRELIMINARY; PRT; 369 AA.  
AC Q9FQM3;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
DE MAP kinase 1 (MAP kinase MAPK5a).  
GN Name=MAPK5;  
OS Oryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzaceae; Oryza.  
OX NCBI\_TaxID=4530;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22167320; PubMed=12177502; DOI=10.1104/pp.006072;  
RA Wen J.Q., Ono K., Imai R.;  
RT "Two novel mitogen-activated protein signaling components, OsMEK1 and  
RT OsMAP1, are involved in a moderate low-temperature signaling pathway  
RT in rice.";  
RL Plant Physiol. 129:1880-1891(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22503591; PubMed=12615946; DOI=10.1105/tpc.008714;  
RA Xiong L., Yang Y.;  
RT "Disease resistance and abiotic stress tolerance in rice are inversely  
RT modulated by an abscisic acid-inducible mitogen-activated protein  
RT kinase.";  
RL Plant Cell 15:745-759(2003).  
DR EMBL; A2216315; AGA40579.1; -; mRNA.  
DR EMBL; AF479883; AAL87689.1; -; mRNA.  
DR HSSP; Q16539; 1KV1.  
DR Gramene; Q9FQM3; -.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004707; F:MAP kinase activity; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR008351; JNK MAPK.  
DR InterPro; IPR003527; MAP kin.  
DR InterPro; IPR000719; Prot kinase.  
DR InterPro; IPR008271; Ser Thr pkin AS.  
DR InterPro; IPR002290; Ser Thr kinase.  
DR Pfam; PF00069; Pkinase; 1.  
DR PRINTS; PR01772; JNKMAPKINASE.

DR ProDom; PD000001; Prot kinase; 2.  
DR SMART; SM00220; S TKC; 1.  
DR PROSITE; PS01351; MAPK; 1.  
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW Kinase.  
SQ SEQUENCE 369 AA; 42995 MW; 417D81732635F2D3 CRC64;  
Query Match 99.5%; Score 1942.5; DB 2; Length 369;  
Best Local Similarity 99.7%; Pred. No. 2.9e-113;  
Matches 368; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 MDGAPVAFRPTMTHTGGRYLLYDIFGNKFEVNTKYQPPIMPIGRGAYGIVCSVMNFETRE 60  
Db 1 MDGAPVAFRPTMTHTGGRYLLYDIFGNKFEVNTKYQPPIMPIGRGAYGIVCSVMNFETRE 60  
QY 61 MVAIKKIANAFNMDAKRTLRKILRLHLDHENIIGIRDVIPPPIPOAFNDVYIATELM 120  
Db 61 MVAIKKIANAFNMDAKRTLRKILRLHLDHENIIGIRDVIPPPIPOAFNDVYIATELM 120  
QY 121 DTDLHHIIRSNOELSEHCQYFLYQILRGLKYIHSANVIHRDLKPSNLLNANCDLKICD 180  
Db 121 DTDLHHIIRSNOELSEHCQYFLYQILRGLKYIHSANVIHRDLKPSNLLNANCDLKICD 180  
QY 181 FGLARPSSESMDMTYVTVTRWYRAPELLNSTDYSAA-DVMSVGCIFMELINRQPLFPGR 239  
Db 181 FGLARPSSESMDMTYVTVTRWYRAPELLNSTDYSAAIDVMSVGCIFMELINRQPLFPGR 240  
QY 240 DHMHQRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIE 299  
Db 241 DHMHQRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIE 300  
QY 300 RMLTFNPLQRIITVEEALDHPYLERLHDIADEPICLEPFSFDFEQKALNEDQMKQLIFNEA 359  
Db 301 RMLTFNPLQRIITVEEALDHPYLERLHDIADEPICLEPFSFDFEQKALNEDQMKQLIFNEA 360  
QY 360 IEMNPNIRY 368  
Db 361 IEMNPNIRY 369  
RESULT 3  
Q9AXF2\_ORYSA  
ID Q9AXF2\_ORYSA PRELIMINARY; PRT; 369 AA.  
AC Q9AXF2;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE MAP kinase BINM1.  
OS Oryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzaceae; Oryza.  
OX NCBI\_TaxID=4530;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Song F., Goodman R.M.;  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF332873; AAK01710.1; -; mRNA.  
DR HSSP; Q16539; 1KV1.  
DR Gramene; Q9AXF2; -.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004707; F:MAP kinase activity; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR008351; JNK MAPK.  
DR InterPro; IPR003527; MAP kin.  
DR InterPro; IPR000719; Prot kinase.  
DR InterPro; IPR008271; Ser Thr pkin AS.  
DR InterPro; IPR002290; Ser Thr kinase.  
DR Pfam; PF00069; Pkinase; 1.  
DR PRINTS; PR01772; JNKMAPKINASE.

DR PRODOM; PD000001; Prot\_kinase; 2.  
 DR SMART; SM00220; S\_TKC; 1.  
 DR PROSITE; PS001351; MAPK; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW Kinase.  
 SQ SEQUENCE 369 AA; 43029 MW; 417D88B32635FD3D3 CRC64;

Query Match 99.3%; Score 1938.5; DB 2; Length 369;  
 Best Local Similarity 99.5%; Pred. No. 5.1e-113;  
 Matches 367; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 MDGAPVAEPRPTMTGGRYLLYDI FGNKFEVTKYOPPIMPICRGAYGIVCSVMNPFETRE 60  
 DB 1 MDGAPVAEPRPTMTGGRYLLYDI FGNKFEVTKYOPPIMPICRGAYGIVCSVMNPFETRE 60

QY 61 MVAIKKIANAFNNDMDAKRTLRKILRLHDHENIIGIRDVIPPPIQAFNDVVIATELM 120  
 DB 61 MVAIKKIANAFNNDMDAKRTLRKILRLHDHENIIGIRDVIPPPIQAFNDVVIATELM 120

QY 121 DTDLHHIIRSNQSLSEHCQYFLYQLRGLKYIHSANVHRDLKPSNLLNANCDLKICD 180  
 DB 121 DTDLHHIIRSNQSLSEHCQYFLYQLRGLKYIHSANVHRDLKPSNLLNANCDLKICD 180

QY 181 FGLARSSSDMTETVYVTRWYRAPELLNSTDYSAA-DVSVGCCIFMELINRQPLPGR 239  
 DB 181 FGLARSSSDMTETVYVTRWYRAPELLNSTDYSAAIDVSVGCCIFMELINRQPLPGR 240

QY 240 DHMQHRLITEVIGTPTDDELGFIRNEDARKYWRHLPOYPRRTFASMPFRVQPAALDLIE 299  
 DB 241 DHMQHRLITEVIGTPTDDELGFIRNEDARKYWRHLPOYPRRTFASMPFRVQPAALDLIE 300

QY 300 RMLTFNPLQRIITVEALDHPYLERLHDADEPICLEPSPDFEQKALNEDQMQLIFNEA 359  
 DB 301 RMLTFNPLQRIITVEALDHPYLERLHDADEPICLEPSPDFEQKALNEDQMQLIFNEA 360

QY 360 IEMNPNIRY 368  
 DB 361 IEMNPNIRY 369

## RESULT 4

Q9FSE6 ORYSA  
 ID Q9FSE6 ORYSA PRELIMINARY; PRT; 369 AA.  
 AC Q9FSE6;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE MAPK2 protein.  
 GN Name=mapk2;  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzoideae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN NCBI\_TaxID=4530;  
 RP NUCLEOTIDE SEQUENCE.  
 RA Huang H.J., Dai Y.H., Huang D.D., Kuo T.T.;  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ250311; CAC13967.1; -; mRNA.  
 DR HSP; Q16539; 1KV1.  
 DR Gramene; Q9FSE6; -.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004707; F:MAP kinase activity; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR008351; JNK MAPK.  
 DR InterPro; IPR003527; MAP kin.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR008271; Ser\_Thr\_pkin\_AS.  
 DR InterPro; IPR002290; Ser\_Thr\_pkinase.  
 DR Pfam; PF00069; Pkinase; 1.

## RESULT 5

Q8GZ23 ORYSA  
 ID Q8GZ23 ORYSA PRELIMINARY; PRT; 357 AA.  
 AC Q8GZ23;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Putative MAP kinase 1.  
 GN Name=OSJNB0013D02.9;  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzoideae; Oryza.  
 OX NCBI\_TaxID=39947;  
 RN NCBI\_TaxID=39947;  
 RP NUCLEOTIDE SEQUENCE.  
 RA Wang R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Currie J.,  
 RA Collura K.;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC134232; AAO16999.1; -; Genomic\_DNA.  
 DR HSP; Q16539; 1KV1.  
 DR Gramene; Q8GZ23; -.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004707; F:MAP kinase activity; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR008351; JNK MAPK.  
 DR InterPro; IPR003527; MAP kin.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR008271; Ser\_Thr\_pkin\_AS.  
 DR InterPro; IPR002290; Ser\_Thr\_pkinase.

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DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR01772; JNKMAPKINASE.
DR ProDom; PD000001; Prot kinase; 2.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS01351; MAPK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase.
SQ SEQUENCE 357 AA; 41723 MW; EF6C054A76B3D8FE CRC64;

Query Match          96.2%; Score 1878.5; DB 2; Length 357;
Best Local Similarity 99.7%; Pred. No. 2.7e-109;
Matches 356; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 13 MTHGGRYLLYDIFGNKFEVNTKYQPPIMPFGAGYGVCSVMNFTREMVAIKKIANAFN 72
DB 1 MTHGGRYLLYDIFGNKFEVNTKYQPPIMPFGAGYGVCSVMNFTREMVAIKKIANAFN 60

QY 73 NDMDAKRTLRREIKLRLHLDHNIIGIRDVIPPPIQAFNDVVIATELMDTDLHHIIRSNQ 132
DB 61 NDMDAKRTLRREIKLRLHLDHNIIGIRDVIPPPIQAFNDVVIATELMDTDLHHIIRSNQ 120

QY 133 ELSEHCQFLYQILRGLKYIHSANVIHRDLKPSNLLNANCDLKICDFGLARPSSESDM 192
DB 121 ELSEHCQFLYQILRGLKYIHSANVIHRDLKPSNLLNANCDLKICDFGLARPSSESDM 180

QY 193 MTEYVTVRWYRAPELLNSTDYSAADVMSVGCIFMELINRQPLPGRDHMHOMRLITEV 251
DB 181 MTEYVTVRWYRAPELLNSTDYSAADVMSVGCIFMELINRQPLPGRDHMHOMRLITEV 240

QY 252 IGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIERMLTFNPLQIRIT 311
DB 241 IGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIERMLTFNPLQIRIT 300

QY 312 VBEALDHPYLERLHDIADSPICLEPSPFDFEQKALNEDQMQLIFNEAIEMNPNI 368
DB 301 VBEALDHPYLERLHDIADSPICLEPSPFDFEQKALNEDQMQLIFNEAIEMNPNI 357

RESULT 6
Q4QWQ7_SACOF
ID Q4QWQ7_SACOF PRELIMINARY; PRT; 370 AA.
AC Q4QWQ7;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Mitogen-activated protein kinase.
OS Saccharum officinarum (Sugar cane).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Saccharum;
OC Saccharum officinarum complex.
OX NCBI_TaxID=4547;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Nogueira P.T.S., Schlogl P.S., Camargo S.R., Fernandez J.H.,
De Rosa V.E. Jr., Pompermayr P., Arruda P.;
"SnNC23, a member of the NAC domain protein family, is associated
with cold, herbivory and water stress in sugarcane.";
RL Plant Sci. 169:93-106(2005).
DR EMBL; AV738652; AAW65993.1; -; mRNA.
KW Kinase.
SQ SEQUENCE 370 AA; 43038 MW; F1C9F29B30A409E CRC64;

Query Match          94.1%; Score 1837; DB 2; Length 370;
Best Local Similarity 94.1%; Pred. No. 1.1e-106;
Matches 348; Conservative 11; Mismatches 9; Indels 2; Gaps 2;

QY 1 MDGAPVAEPRPTWTHGGRVLLYDIFGNKFEVNTKYQPPIMPFGAGYGVCSVMNFTRE 60
DB 1 MDGAPVAEPRPTWTHGGRVLLYDIFGNKFEVNTKYQPPIMPFGAGYGVCSVMNFTRE 60

QY 61 MVAIKKIANAFNNDMDAKRTLRREIKLRLHLDHNIIGIRDVIPPPIQAFNDVVIATELM 120
DB 61 MVAIKKIANAFNNDMDAKRTLRREIKLRLHLDHNIIGIRDVIPPPIQAFNDVVIATELM 120

QY 121 DTDLHHIIRSNQELSEHCQFLYQILRGLKYIHSANVIHRDLKPSNLLNANCDLKICD 180
DB 121 DTDLHHIIRSNQELSEHCQFLYQILRGLKYIHSANVIHRDLKPSNLLNANCDLKICD 180

QY 181 FGLARPSSESDMTEYVTVRWYRAPELLNSTDYSAADVMSVGCIFMELINRQPLPGR 239
DB 181 FGLARPSSESDMTEYVTVRWYRAPELLNSTDYSAADVMSVGCIFMELINRQPLPGR 240

QY 240 DHMHQMLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLI 298
DB 241 DHMHQMLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLI 300

QY 299 ERMLTFNPLQIRITVBEALDHPYLERLHDIADSPICLEPSPFDFEQKALNEDQMQLIFNE 358
DB 301 ERMLTFNPLQIRITVBEALDHPYLERLHDIADSPICTEPSPFDFEQKALNEDQMQLIFNE 360

QY 359 AIEMNPNI 368
DB 361 AIEMNPNI 370

RESULT 7
Q43379_AVESA
ID Q43379_AVESA PRELIMINARY; PRT; 369 AA.
AC Q43379;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MAP KINASE.
GN Name=Asmapi;
OS Avena sativa (Oat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Aveneae; Avena.
OX NCBI_TaxID=4498;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Huttly A.K., Phillips A.L.;
"ghberellin regulated expression in oat aleurone cells of two kinases
that hsw homology to nap kinase and a ribosomal protein kinase.";
RL Plant Mol. Biol. 27:1043-1052(1995).
DR EMBL; X79993; CAA56314.1; -; mRNA.
DR PIR; S56638; S56638.
DR HSP; Q16539; 1KV1.
DR Gramene; Q43379; -.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0004707; P:MAP kinase activity; IEA.
DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR008351; JNK MAPK.
DR InterPro; IPR003527; MAP_kin.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR01772; JNKMAPKINASE.
DR ProDom; PD000001; Prot kinase; 2.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS01351; MAPK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase; Serine/threonine-protein_kinase.
SQ SEQUENCE 369 AA; 42871 MW; 2A76A350A867A63F CRC64;

Query Match          93.2%; Score 1819.5; DB 2; Length 369;
Best Local Similarity 91.3%; Pred. No. 1.3e-105;

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Matches 337; Conservative 20; Mismatches 11; Indels 1; Gaps 1;

QY 1 MDGAPVAEPRPTMTTHGGRVLLYDIFGNKEFEVNTKYPPIPIGRGAYGIVCSVMNPETRE 60  
 DB 1 MDGAPVAEPRPTMTTHGGRVLLYDIFGNKEFEVNTKYPPIPIGRGAYGIVCSVMNPETRE 60

QY 61 MVAIKKIANAFNNDMDAKETLREIKLRLHLDHENIIGIRDVIPPPIPOAFNDVVIATELM 120  
 DB 61 MVAIKKIANAFNNDMDAKETLREIKLRLHLDHENIIGIRDVIPPPIPOAFNDVVIATELM 120

QY 121 DTDLHHIIRSNQELSEHCQFYQLRLGKYIHSANVTHRDLPKSNLLNANCDLKICD 180  
 DB 121 DTDLHHIIRSNQELSEHCQFYQLRLGKYIHSANVTHRDLPKSNLLNANCDLKICD 180

QY 181 FGLARPSSESDMMTEVYVTRWYRAPELLNSTDYSAA-DVWSVGCIFMELINRQPLPPGR 239  
 DB 181 FGLARPSSESDMMTEVYVTRWYRAPELLNSTDYSAAIDVWSVGCIFMELINRQPLPPGR 240

QY 240 DHMHQRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPRVQPAALDLIE 299  
 DB 241 DHMHQRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPRVQPAALDLIE 300

QY 300 RMLTFNPLQRIITVEEALDHPYLERLHDADEPCLPFPFDFQKALNEDQMKQLIFNEA 359  
 DB 301 RMLTFNPLQRIITVEEALDHPYLERLHDADEPCLPFPFDFQKALNEDQMKQLIFNEA 360

QY 360 IEMNPNIY 368  
 DB 361 LELNPNFNY 369

RESULT 8

ID O81599 WHEAT PRELIMINARY; PRT; 369 AA.

AC O81599;

DT 01-NOV-1998 (TrEMBLrel. 08, Created)

DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE MAP kinase homolog.

GN Names=WCK-1;

OS Triticum aestivum (Wheat).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;

OC Triticeae; Triticum.

OX NCBI\_TaxID=4565;

[1]

RN NUCLEOTIDE SEQUENCE.

RP STRAIN=Chihokumugi;

RC MEDLINE=99454541; PubMed=10527417; DOI=10.1023/A:1006263607135;

RX Takezawa D.;

RT "Elicitor- and A23187-induced expression of WCK-1, a gene encoding

RT mitogen-activated protein kinase in wheat.";

RL Plant Mol. Biol. 40:921-933(1999).

DR EMBL; AF079318; AAC28850.1; -; mRNA.

DR HSP; Q16539; IKV1.

DR Gramene; O81599; -.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0004707; F:MAP kinase activity; IEA.

DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

DR InterPro; IPR008351; JNK\_MAPK.

DR InterPro; IPR003527; MAP\_Kin.

DR InterPro; IPR00719; Prot kinase.

DR InterPro; IPR008271; Ser Thr\_pkin\_AS.

DR InterPro; IPR002290; Ser Thr\_pkinase.

DR Pfam; PF00069; Pkinase; I.

DR PRINTS; PR01772; JNKMAPKINASE.

DR PRODOM; PD000001; Prot kinase; 2.

DR SMART; SM00220; S\_TKc; 1.

DR PROSITE; PS01351; MAPK; 1.

DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.

DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.

KW Kinase.

QY 1 MDGAPVAEPRPTMTTHGGRVLLYDIFGNKEFEVNTKYPPIPIGRGAYGIVCSVMNPETRE 60  
 DB 1 MDGAPVAEPRPTMTTHGGRVLLYDIFGNKEFEVNTKYPPIPIGRGAYGIVCSVMNPETRE 60

QY 61 MVAIKKIANAFNNDMDAKETLREIKLRLHLDHENIIGIRDVIPPPIPOAFNDVVIATELM 120  
 DB 61 MVAIKKIANAFNNDMDAKETLREIKLRLHLDHENIIGIRDVIPPPIPOAFNDVVIATELM 120

QY 121 DTDLHHIIRSNQELSEHCQFYQLRLGKYIHSANVTHRDLPKSNLLNANCDLKICD 180  
 DB 121 DTDLHHIIRSNQELSEHCQFYQLRLGKYIHSANVTHRDLPKSNLLNANCDLKICD 180

QY 181 FGLARPSSESDMMTEVYVTRWYRAPELLNSTDYSAA-DVWSVGCIFMELINRQPLPPGR 239  
 DB 181 FGLARPSSESDMMTEVYVTRWYRAPELLNSTDYSAAIDVWSVGCIFMELINRQPLPPGR 240

QY 240 DHMHQRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPRVQPAALDLIE 299  
 DB 241 DHMHQRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPRVQPAALDLIE 300

QY 300 RMLTFNPLQRIITVEEALDHPYLERLHDADEPCLPFPFDFQKALNEDQMKQLIFNEA 359  
 DB 301 RMLTFNPLQRIITVEEALDHPYLERLHDADEPCLPFPFDFQKALNEDQMKQLIFNEA 360

QY 360 IEMNPNIY 368  
 DB 361 LELNPNFNY 369

RESULT 9

ID Q9ZMJ6 MAIZE PRELIMINARY; PRT; 406 AA.

AC Q9ZMJ6;

DT 01-MAY-1999 (TrEMBLrel. 10, Created)

DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE MAP kinase 4.

GN Names=ZmMPK4;

OS Zea mays (Maize).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC PACCAD clade; Panicoideae; Andropogoneae; Zea.

OX NCBI\_TaxID=4577;

[1]

RN NUCLEOTIDE SEQUENCE.

RP STRAIN=honeybuntam;

RC MEDLINE=20055759; PubMed=10589842; DOI=10.1007/s004380051115;

RX Berberich T., Sano H., Kusano T.;

RT "Involvement of a MAP kinase, ZmMPK5, in senescence and recovery from

RT low-temperature stress in maize.";

RL Mol. Gen. Genet. 262:534-542(1999).

CC -|- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

DR EMBL; AB016801; BAA74733.1; -; mRNA.

DR HSP; Q16539; IKV1.

DR Gramene; Q9ZMJ6; -.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0004707; F:MAP kinase activity; IEA.

DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

DR InterPro; IPR008351; JNK\_MAPK.

DR InterPro; IPR00719; Prot kinase.

DR InterPro; IPR008271; Ser Thr\_pkin\_AS.

DR InterPro; IPR002290; Ser Thr\_pkinase.

DR Pfam; PF00069; Pkinase; I.

DR PRINTS; PR01772; JNKMAPKINASE.

[illegible]

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RESULT 10
QSK6Q4_SOYBN
ID QSK6Q4 SOYBN PRELIMINARY; PRT; 371 AA.
AC QSK6Q4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Mitogen-activated protein kinase 1.
GN Name=MAPK1;
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; rosids;
OC eucosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
NCBI_TaxID=3847;
RX [1]
RN NUCLEOTIDE SEQUENCES.
RP Daxberger A., Mithoefer A., Nemak A., Hirt H., Ebel J.;
RA "Elicitor-activated mitogen-activated protein kinase(s) (MAPK) from
RT soybean (Glycine max L.)";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF104247; AAQ13491.1; -; mRNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004707; F:MAP kinase activity; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006458; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR008351; UNK MAPK.
DR InterPro; IPR003527; MAP_kin.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin AS.

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[illegible]

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RESULT 11
Q9M6S1_PEA PRELIMINARY; PRT; 371 AA.
Q9M6S1;
AC Q9M6S1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MAP kinase 3.
GN Name=Mapk3;
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; core eudicotyledons;
OC rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OX NCBI_TaxID=3888;
[1]
RN NUCLEOTIDE SEQUENCE.
RS TISSUE=Ovary;
RC MEDLINE=21003323; PubMed=11117263; DOI=10.1023/A:1006434330381;
RA Marcote M.J., Carbonell J.;
RT "Transient expression of a pea MAP kinase gene induced by gibberellic
acid and 6-benzyladenine in unpollinated pea ovaries.";
RL Plant Mol. Biol. 44:177-186(2000).
RS EMBL; AF153061; AAF73236.1; -; mRNA.
DR HSPSP; Q16539; 1KVP1.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0004707; P:MAP kinase activity; IEA.
DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR008351; JNK MAPK.
DR InterPro; IPR003527; MAP_kin.
DR InterPro; IPR000719; Prot_kinase.

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DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR01772; JNKMAPKINASE.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS01351; MAPK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase.
SQ SEQUENCE 371 AA; 42919 MW; A6F422D295CF488C CRC64;

Query Match 77.1%; Score 1505.5; DB 2; Length 371;
Best Local Similarity 74.7%; Pred. No. 5e-86;
Matches 269; Conservative 55; Mismatches 35; Indels 1; Gaps 1;

QY 6 VAEFRPTMTGGRYLLDIFGNKFEVTNKYQPPIMPIGRGAYGIVCSVMNFETREMVAK 65
DB 9 VAEFPVQTHGGQFVQNVFGNLFEVTAKYRPPIMPIGRGAYGIVCSLLTNETNELVAK 68
QY 66 KIANAFNDMDAKRTLEIKLARHLDHENIIGIRDVIPPPIQAFNDVVIATLMDTDLH 125
DB 69 KIANAFDNDMDAKRTLEIKLARHLDHENVIGLRDVIPLPREFNDVITTELMDTDLH 128
QY 126 HIIRSQELSEHCQFYQLRGLKYIHSANVIHRDLKPSNLLNANCDLKI CDFGLAR 185
DB 129 QIIRSNQNLSDHCQFYQLRGLRYIHSANIIHRDLKPSNLLNANCDLKI CDFGLAR 188
QY 186 PSESMDMTYVYVTRWYRAPELLNSTDY- SAADVMSVGCIFMELNRPPLPGRDHMQ 244
DB 189 PTMENDFMTEYVYVTRWYRAPELLNSTDYSAIDVMSVGCIFMELNKKPLPFGKDHVQ 248
QY 245 MRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPRPVQPAALDIERM LTF 304
DB 249 MRLITELLGPTDADVLGVKNEDARYIRQLPQYRQPLNRVPHVPLAIDLIDKMLTI 308
QY 305 NPLQRTVTEALDHPYLERLHDIADPICLEPSPDFEQKALNEDQKQLIFNEAIE MNP 364
DB 309 DPTRRITVEALAHPLYLEKLDHVADEPICMEPSPDFEQQHLDEEIKEMIVREALANP 368

RESULT 12
O24077 MEDSA
ID O24077 MEDSA PRELIMINARY; PRT; 371 AA.
AC O24077;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Protein kinase.
GN Name=MKK4;
OS Medicago sativa (Alfalfa).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
OC Medicago.
OX NCBI_TaxID=3879;
RN [1]
RP NUCLEOTIDE SEQUENCE
RX MEDLINE=97008170; PubMed=8853346; DOI=10.1073/pnas.93.20.11274;
RA Jonak C., Kiegiel S., Ligttering W., Barker P., Huskisson N., Hirt H.;
RT "signaling in plants: a mitogen-activated protein kinase pathway is
RT activated by cold and drought."
RL Proc. Natl. Acad. Sci. U.S.A. 93:11274-11279(1996).
DR EMBL; X82270; CAA57721.1; -, mRNA.
DR FRR; T09622; T09622.
DR HSP; Q16539; Ikv1.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004707; F:MAP kinase activity; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR008351; JNK MAPK.
DR InterPro; IPR003527; MAP_kin.

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DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR01772; JNKMAPKINASE.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS01351; MAPK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase.
SQ SEQUENCE 371 AA; 42963 MW; 8CCC390454E4350E CRC64;

Query Match 77.0%; Score 1504.5; DB 2; Length 371;
Best Local Similarity 74.4%; Pred. No. 5.8e-86;
Matches 268; Conservative 56; Mismatches 35; Indels 1; Gaps 1;

QY 6 VAEFRPTMTGGRYLLDIFGNKFEVTNKYQPPIMPIGRGAYGIVCSVMNFETREMVAK 65
DB 9 VAEFPVQTHGGQFVQNVFGNLFEVTAKYRPPIMPIGRGAYGIVCSLLTNETNELVAK 68
QY 66 KIANAFNDMDAKRTLEIKLARHLDHENIIGIRDVIPPPIQAFNDVVIATLMDTDLH 125
DB 69 KIANAFDNDMDAKRTLEIKLARHLDHENVIGLRDVIPLPREFNDVITTELMDTDLH 128
QY 126 HIIRSQELSEHCQFYQLRGLKYIHSANVIHRDLKPSNLLNANCDLKI CDFGLAR 185
DB 129 QIIRSNQNLSDHCQFYQLRGLRYIHSANIIHRDLKPSNLLNANCDLKI CDFGLAR 188
QY 186 PSESMDMTYVYVTRWYRAPELLNSTDY- SAADVMSVGCIFMELNRPPLPGRDHMQ 244
DB 189 PTMENDFMTEYVYVTRWYRAPELLNSTDYSAIDVMSVGCIFMELNKKPLPFGKDHVQ 248
QY 245 MRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPRPVQPAALDIERM LTF 304
DB 249 MRLITELLGPTDADVLGVKNEDARYIRQLPQYRQPLNRVPHVPLAIDLIDKMLTI 308
QY 305 NPLQRTVTEALDHPYLERLHDIADPICLEPSPDFEQKALNEDQKQLIFNEAIE MNP 364
DB 309 DPTRRITVEALAHPLYLEKLDHVADEPICMEPSPDFEQQHLDEEIKEMIVREALANP 368

RESULT 13
Q8W406 TOBAC
ID Q8W406 TOBAC PRELIMINARY; PRT; 375 AA.
AC Q8W406;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Wound induced protein kinase.
GN Name=WIPK;
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP NUCLEOTIDE SEQUENCE
RA Sano H., Yap Y.K.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AB052964; BAB79636.1; -, Genomic_DNA.
DR HSP; Q16539; Ikv1.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004707; F:MAP kinase activity; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR003527; MAP_kin.
DR InterPro; IPR008352; p38_MAPK.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.

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DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR01773; P38MAPKINASE.
DR ProDom; PD00001; Prot_kinase; 2.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS01351; MAPK; UNKNOWN 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 375 AA; 42898 MW; 9BA49C839E1C86F CRC64;

Query Match 75.9%; Score 1481.5; DB 2; Length 375;
Best Local Similarity 73.0%; Pred. No. 1.6e-84;
Matches 265; Conservative 55; Mismatches 42; Indels 1; Gaps 1;

QY 3 GAPVAEPRPTWTHGGRYLLYDIFGNKFEVTKYQPIPIGRGAYGIVCSVMNFEETREMV 62
DB 10 GGOFPDPFVSLTHGGYQYQDIFGNFETTKYRPPIMPPIGRGAYGIVCSVLNTELMNV 69
QY 63 AIKKIANAFNNDMDAKRTLREIKLRLHLDHENIIGIRDVIPPPIPOAFNDVVIATELMDT 122
DB 70 AVKIANAFNDYMDAKRTLREIKLRLHLDHENVIGLRDVIPLPLRREFSDVVIATELMDT 129
QY 123 DLHIIIRSNQELSEHCQYFLYQILRGLKYIHSANVIHRDLKPSNLLNANCDLKICDPG 182
DB 130 DLHIIIRSNQGLSEHCQYFMYQLLRLGLKYIHSANVLRDLKPSNLLNANCDLKICDPG 189
QY 183 LARPSSESDMTVEYVTRVYRAPELLNSTDYSA-DVMSVGCIFMELINRPLPFGRDH 241
DB 190 LARPNLENEMTEYVTRVYRAPELLNSTDYTAADVMSVGCIFMELNRRKPLFAGKDH 249
QY 242 MHQRLITVEIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPRVQPAALDLIERM 301
DB 250 VHQIRLLTFLGTPTDELGFQNEADAKYIIRQLPQHPQQLAEVPPHVNPLAIDLVDKM 309
QY 302 LTFNPLQRIITVEALDHPYLERLHDIADSPICLEPFSDFEQKALNEDQMQLIFNEAIE 361
DB 310 LTLDPFRRITVEALDHPYLERLHDIADSPICLPVPPSDFEQGIGEEIKDMIQEALS 369
QY 362 MNP 364
DB 370 LNP 372

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RESULT 14
Q51V18 BRANA
ID Q51V18_BRANA PRELIMINARY; PRT; 370 AA.
AC Q51V18;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Mitogen-activated protein kinase 3.
OS Brassica napus (Rapel).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RA Yu S., Zhang L., Zuo K., Tang D., Tang K.;
RT "Isolation and characterization of an oilseed rape MAP kinase BnMPK3
involved in diverse environmental stresses.";
RL Plant Sci. 169:413-421(2005).
DR EMBL; AY642433; RAU34677.1; -; mRNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004707; F:MAP kinase activity; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR008350; Erk_3_4_MAPK.
DR InterPro; IPR008351; JNK_MAPK.

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DR InterPro; IPR003527; MAP_kin.
DR InterPro; IPR00719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_kin AS.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR01771; ERK3ERK4MAPK.
DR PRINTS; PR01772; JNKMAPKINASE.
DR ProDom; PD00001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS01351; MAPK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase.
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Query Match 75.8%; Score 1480.5; DB 2; Length 370;
Best Local Similarity 73.8%; Pred. No. 1.8e-84;
Matches 268; Conservative 54; Mismatches 40; Indels 1; Gaps 1;

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DB 5 GGOYDPFPAVQTHGGQFISYDIFGSLFVTSKYRPPIVPIGRGAYGIVCSVLDSSTNELV 64
QY 63 AIKKIANAFNNDMDAKRTLREIKLRLHLDHENIIGIRDVIPPPIPOAFNDVVIATELMDT 122
DB 65 AMKIANAFNDMDAKRTLREIKLRLHLDHENIIRDVVPPPLRREFSDVVIATELMDT 124
QY 123 DLHIIIRSNQELSEHCQYFLYQILRGLKYIHSANVIHRDLKPSNLLNANCDLKICDPG 182
DB 125 DLHIIIRSNQGLSEHCQYFLYQILRGLKYIHSAKVIHRDLKPSNLLNANCDLKICDPG 184
QY 183 LARPSSESDMTVEYVTRVYRAPELLNSTDYSA-DVMSVGCIFMELINRPLPFGRDH 241
DB 185 LARPTSENEFTEYVTRVYRAPELLNSTDYTAADVMSVGCIFMELNRRKPLPFGKDH 244
QY 242 MHQRLITVEIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPRVQPAALDLIERM 301
DB 245 VHQRELLTFLGTPTESDLGFTHNEDAKYIRQLPNPFRQPLAKLFSHVNSLAIDLVDKM 304
QY 302 LTFNPLQRIITVEALDHPYLERLHDIADSPICLEPFSDFEQKALNEDQMQLIFNEAIE 361
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DB 365 LNP 367

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DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mitogen-activated protein kinase 3.
GN Name=MPK3;
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; lamiales; Solanaceae; Solanaceae; Solanum; Lycopersicon.
OX NCBI_TaxID=4081;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=22795301; PubMed=12913131; DOI=10.1104/pp.103.024414;
RX Holley S.R., Yamanchili R.D., Moura D.S., Ryan C.A., Stratman J.W.;
RT "Convergence of signaling pathways induced by systemin,
oligosaccharide elicitors and ultraviolet-B radiation at the level of
mitogen-activated protein kinases in Lycopersicon peruvianum
suspension-cultured cells.";

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model  
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(without alignments)  
16163.021 Million cell updates/sec

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Perfect score: 1396  
Sequence: 1 agagagtcagataaggtcgt.....ttaaaaaaaaaaaaaaaaaa 1396

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_hic:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_est7:\*  
9: gb\_gsa1:\*  
10: gb\_gsa2:\*  
11: gb\_gsa3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	1072.4	76.8	1074	10	CL961355 OsIFCC006
2	755	54.1	755	6	CB675228 OSJNBE10N
3	748.8	53.6	752	6	CB675229 OSJNBE10N
4	725	51.9	1031	7	CK163044 FGAS01565
5	668.2	47.9	863	2	BE412950 MCG016.H0
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7	654.6	46.9	921	8	DR792177 ZM_BF001
8	623.2	44.6	859	7	CN130436
9	611.4	43.8	718	6	CA213307
10	608	43.6	632	7	CK077805
11	606.4	43.4	608	5	C99344
12	603.8	43.3	819	6	CF243446
13	595.4	42.7	700	1	AL504341
14	594.2	42.6	667	3	BI805515
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16	590.8	42.3	806	7	CO527096
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18	579.4	41.5	648	6	CA272118
19	578.4	41.4	949	6	CA150824
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	24	563.6	40.4	654	6	CA485025	CA485025 WHE4313 E
	25	561.4	40.2	814	8	DR811341	DR811341 ZM_BF0003
	26	560.8	40.2	768	6	CA159385	CA159385 SCUPR23C0
	27	559.4	40.1	783	8	DR787175	DR787175 ZM_BF0000
	28	555.4	39.8	857	7	CN130591	CN130591 RHOH1 42
	29	550	39.4	1004	7	CO731261	CO731261 JMW019E02
	30	549	39.3	775	8	DR813762	DR813762 ZM_BF0004
	31	547.4	39.2	590	7	CR292974	CR292974 CR292974
	32	546	39.1	675	7	CV071886	CV071886 EST4047 Z
	33	541.6	38.8	819	7	CK199849	CK199849 FGAS00835
	34	536.6	38.4	600	6	CA484243	CA484243 WHE4304 A
	35	535.8	38.4	771	8	DR972294	DR972294 ZM_BF0009
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	37	533.6	38.2	651	7	CF920113	CF920113 EST4413 Z
	38	532.4	38.1	1499	8	CX099485	CX099485 REC0052
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	42	520.8	37.3	1715	4	AY108471	AY108471 Zea mays
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## ALIGNMENTS

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LOCUS CL961355 1074 bp DNA linear GSS 21-SEP-2004  
DEFINITION OsIFCC006088 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.  
ACCESSION CL961355  
VERSION CL961355.1 GI:52377449  
KEYWORDS GSS.  
SOURCE Oryza sativa (indica cultivar-group)  
ORGANISM Oryza sativa (indica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
REFERENCE 1 (bases 1 to 1074)  
AUTHORS Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M., Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L., Wong, G.K.S., Deng, X.W. and Wang, J.  
TITLE An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis  
JOURNAL Unpublished (2004)  
COMMENT Contact: Chen Chen  
Department of Bioinformatic  
Beijing Institute of Genomics  
Chinese Academy of Sciences, Beijing 101300, China  
Tel: 86-10-80481559  
Fax: 86-10-80488676  
Email: chenchen@genomics.org.cn  
Rice genomic sequence.  
Class: exon-trapped.  
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Location/Qualifiers  
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Matches 1073; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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Db 1 ATGACGACGCGCGCGGTACCTCTACGACATCTTCGGGAACAAGTTCGAGGTACG 60  
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QY 234 GTGATGAATTTTGAGACGAGGAGATGTTGGCGATTAAGAAGATGCCCAACGGTTTCAAC 293
DB |||
DB 121 GTGATGAATTTTGAGACGAGGAGATGTTGGCGATTAAGAAGATGCCCAACGGTTTCAAC 180
QY 294 AACGACATGGACGCCAAGCGCAGCTCCGGGAGATCAAGCTCTCGAGCACTCGACCA 353
DB |||
DB 181 AACGACATGGACGCCAAGCGCAGCTCCGGGAGATCAAGCTCTCGAGCACTCGACCA 240
QY 354 GAGAACATCATAGGCATCAGGATGTGATCCGCCCGCATCTCCAGCGGTTCAACGAC 413
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DB 241 GAGAACATCATAGGCATCAGGATGTGATCCGCCCGCATCTCCAGCGGTTCAACGAC 300
QY 414 GTCTACATCGCCACGAGCTCATGGACACGACCTCCATCATCATCATCTCCCAACCA 473
DB |||
DB 301 GTCTACATCGCCACGAGCTCATGGACACGACCTCCATCATCATCATCTCCCAACCA 360
QY 474 GAACTGTACAGACGACCTGCCAGTATTTCTGTACAGATCTGCGGGGCTCAAGTAC 533
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DB 361 GAACTGTACAGACGACCTGCCAGTATTTCTGTACAGATCTGCGGGGCTCAAGTAC 420
QY 534 ATCCACTCGCGCAACGTGATCCACCGCGACCTGAAGCCGAGCAACCTGCTGTGAACGCC 593
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DB 421 ATCCACTCGCGCAACGTGATCCACCGCGACCTGAAGCCGAGCAACCTGCTGTGAACGCC 480
QY 594 AACTGCGACCTCAAGATCTGCGATTTGCGGCTGGCGCGCTGCTGCGAGAGGACATG 653
DB |||
DB 481 AACTGCGACCTCAAGATCTGCGATTTGCGGCTGGCGCGCTGCTGCGAGAGGACATG 540
QY 654 ATGACGAGTACGTGTCTACCCGGTGTACCCGCGCGCGGAGCTGTCTCACTCCACC 713
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DB |||
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QY 774 CGCCAGCGCTTTCCCGCGAGGACCAATGCAACAGATGCGCTCATCAACCGAGGTG 833
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QY 834 ATCGGAGCGCGAGCGAGCTGGGTTTCATAGGAAACGAGACCGGAGGATAC 893
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QY 894 ATGAGGCACCTGCGCAGTACCGCGCGGAGCTTCGCGAGCATGTTCCCGGGTGCA 953
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RESULT 2

CB675228

LOCUS

CB675228 755 bp mRNA linear EST 09-APR-2003

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clone OSJNEe10N07 5', mRNA sequence.
ACCESSION CB675228
VERSION CB675228.1 GI:29678953
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 755)
AUTHORS Jantassuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
TITLE Large-scale identification of expressed sequence tags involved in
rice and rice blast fungus interaction
JOURNAL Plant Physiol. 138 (1), 105-115 (2005)
PUBMED 15886893
COMMENT Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 10 row: N column: 07
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DB 61 GTACGAGCGGCCCATCATGCCATTGGCGCGCGCCTACGGGATGCTGTCTCGTGAT 120
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DB 121 GAACTTTGAGACGAGGAGATGTTGGCGATTAAGAAGATCGCCACGCGTTCAACACGA 180
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DB 181 CATGAGCGCAAGCGCAGCTCCGGGAGATCAAGCTCTCAGGACCTCGACACGAGAA 240
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RESULT 3  
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DEFINITION  
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clone OSJNBe10N07 3', mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
COMMENT

CB675229 752 bp mRNA linear EST 09-APR-2003  
OSJNBe10N07 3', mRNA sequence.  
CB675229  
CB675229.1 GI:29678954  
EST.  
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Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Erihartoideae; Oryzeae; Oryza.  
1 (bases 1 to 752)  
Jantaseuriyat,C., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,  
Soderlund,C. and Wang,G.L.  
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,  
Large-scale identification of expressed sequence tags involved in  
rice and rice blast fungus interaction  
Plant Physiol. 138 (1), 105-115 (2005)  
1588683  
Contact: Rod Wing  
Arizona Genomics Institute  
University of Arizona  
Biological Sciences West, 449A, P.O. Box 210088, Tucson, AZ  
85721-0088, USA  
Tel: 520 626 3967  
Fax: 520 621 9288  
Email: rwing@genome.arizona.edu  
PCR Primers  
FORWARD: gta aaa cga cgg cca gtc  
BACKWARD: gga aac agc tat gac cat g  
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Db 572 CCACATGCACACGATGCGCTTCATCACCGAGGTGATCGGGAGCGCGACGACGAGCT 513  
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QY 920 CCGGAGTTTCGCGAGCATGTTCCCGGGTGCAGCGCGCGCTCGACCTCATCGAGAG 979  
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Db 392 GATGCTCACCTTCAACCCCGCTGCAGAGAATCAAGTTGAGGAGCGCTCGATCATCTTA 333  
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Db 272 CTTGAGGAGGAGGCTCTTAAACGAGGACCAAAATGAAGCAGCTGATCTTCAACGAAGCAT 213  
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RESULT 4  
CK163044  
LOCUS  
DEFINITION  
FGAS015659 Triticum aestivum FGAS: Library 4 Gate 8 Triticum  
aestivum cDNA, mRNA sequence.  
CK163044  
CK163044.1 GI:38992873  
KEYWORDS  
SOURCE  
ORGANISM  
Triticum aestivum (bread wheat)  
Triticum aestivum



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FEATURES
  source      Location/Qualifiers
 1. .863
  /organism="Hordeum vulgare"
  /mol_type="mRNA"
  /db_xref="taxon:4513"
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  /dev_stage="etiolated"
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ORIGIN
Query Match      47.9%; Score 668.2; DB 2; Length 863;
Best Local Similarity 89.6%; Pred. No. 2e-145;
Matches 715; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 219 GGGATCGTCTGCTCCGGTATGAATTTGAGACGAGGAGATGTTGGCGATTAAGAAGATC 278
DB 17 GGNATCGTCTGCTCGGTGATGAATTCGACACGAGGAGATGNGGCAATCAAGAAGATC 76
QY 279 GCCAACCGCTTCAACAACGACATGAGCGCCCAAGGCGACGCTCCGGGAGATCAAGCTCCTC 338
DB 77 GCAACGCGCTTCGACACAAACATGGAGCGCCCAAGCGCACGCTCCGGGAAATCAAACTCCTC 136
QY 339 AGGCACCTCGACACGAGACATCATAGGATCAGGATGATGATCCCGCGCGATCCCT 398
DB 137 AAGACCTCGACACGAGAAACATAGTAGGCTCCGAGACGTGATCCCGCGCGATCCCG 196
QY 399 CAGGCGCTTCAACGACGCTCTACATCGCCACGCGAGCTCATGACACCGACCTCCCATCATC 458
DB 197 CAGTCTTCAACGACGCTCTACATCGCCACCTGAGCTCATGACACCGACCTTCAACCATC 256
QY 459 ATCCGCTTCAACCAAGAACTGTGAGAGAGACATGCCAGTATTTCTTGATACAGATCCTG 518
DB 257 ATCCGCTTCAACCAAGAACTGTGAGAGAAACATGCCAGTATTTCTTGATACAGATCCTG 316
QY 519 CGGGGCTCAAGTACATCCTACTCGGGAAGTGTATCCACCGACCTCGAAGCGAGCAAC 578
DB 317 CGGGGCTCAAGTACATCCTACTCGGGAAGTGTATCCACCGACCTCGAAGCGAGCAAC 376
QY 579 CTGCTGCTGAACGCAACTCGACCTCAAGATCTCGACCTTCCGGCTTGGCGCGCGCTCG 638
DB 377 CTGCTGCTGAACGCAACTCGACCTCAAGATCTCGACCTTCCGGCTTGGCGCGCGCTCG 436
QY 639 TCGGAGAGCGACATGATGACGAGTACGAGTACCCGGTGTACCCGGTGTACCCGGCGCGAGCTG 698
DB 437 TCGGAGAGCGACATGATGACGAGTACGAGTACCCGGTGTACCCGGTGTACCCGGCGCGAGCTG 496
QY 699 CTGCTCAACTCCACCGACTACTCCGCGCCATCGACGTCTGCTCGTCCGCTGCATCTTC 758
DB 497 CTGCTCAACTCCACCGACTACTCCGCGCCATCGACGTCTGCTCGTCCGCTGCATCTTC 556
QY 759 ATGAGGCTCATCAACCCGCGAGCGCTCTTCCCGGACGAGGACACATGACACAGATCGCG 818
DB 557 ATGAGGCTCATCAACCCGCGAGCGCTCTTCCCGGAGGAGGACACATGACACAGATCGCG 616
QY 819 CTATATCCAGAGTGTATCGGAGACCGCGACGAGCGAGATGAGGTTTATATCGGAACGAG 878
DB 617 CTATATCCAGAGTGTATCGGAGACCGCGACGAGCGAGATGAGGTTTATATCGGAACGAG 676
QY 879 GAGCGAGGAGTATCATGAGGACCTCGCGAGTACCGCGAGGAGTTCGGGAGCATG 938
DB 677 GAGCGAGGAGTATCATGAGGACCTCGCGAGTTCCTCGCGGCGGTTTCCCGGCGAGT 736
QY 939 TTCCCGGCGGTGACAGCCGCGCGCTCGACCTCATCGAGAGGATGCTCAGCTTCAACCCG 998
DB 737 TCCCAAGGTGCAAGNCAGCGCGCTCGACCTCATAGAGCGGATGCTTACCTTCAACCCG 796
QY 999 CTGAGAGAAATCACAGTT 1016
DB 797 NTTGAGAGGATCACAGGT 814

RESULT 6
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QY 708 TCCACCGACTACTCCGCGCCATCGAGCTCTGCTCGTGGCTGCATCTTCATGGAGCTC 767
DB 784 TCCACCGACTACTCCGCGCCATCGAGCTCTGCTCGTGGCTGCATCTTCATGGAGCTC 843
QY 768 ATCAACCGCCAGCGCTCTTCCCGGAGGAGCACATGACACAGATGCGCCTCATCACC 827
DB 844 AATCACCGCCAGCGCTCTTCCCGGAGGAGCACATGACACAGATGCGCCTCATACCC 903
QY 828 GAGGTGATCGGAGGCC 844
DB 904 GAGGTGATCGGAGGCC 920

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RESULT 8  
CN130436  
LOCUS  
DEFINITION  
RHOH1\_41\_B01.g1\_A002 Acid- and alkaline-treated roots Sorghum EST 01-APR-2004  
bicolor cDNA clone RHOH1\_41\_B01\_A002 5', mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Sorghum bicolor (sorghum).  
Sorghum bicolor  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD  
clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE  
AUTHORS  
1 (bases 1 to 859)  
Sun, F., Sullivan, R., Lim, S., Eastman, A. and Pratt, L.H.  
An EST database from Sorghum: acid- and alkaline-treated roots  
Unpublished (2003)

TITLE  
JOURNAL  
COMMENT  
Other ESTs: RHOH1\_41\_B01.b1\_A002  
Contact: Cordonnier-Pratt MM  
Laboratory for Genomics and Bioinformatics  
The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 583 0210  
Email: mmpratt@uga.edu

Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in  
the Human Genome Center, University of Tokyo Institute of Medical  
Science; plant material and RNA prepared at Texas A & M University;  
sequencing done in the Laboratory for Genomics and Bioinformatics,  
University of Georgia. Sequence ends have been trimmed to exclude  
vector and regions below Phred quality 16. Three-prime sequences  
are presented as their reverse complement and have been trimmed to  
exclude polyA.  
Seq primer: Sug5 (CTTCTGCTCTAAAGCTCG).

FEATURES  
source  
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location/Qualifiers  
/organism="Sorghum bicolor"  
/mol\_type="mRNA"  
/cultivar="BTx623"  
/db\_xref="taxon:4558"  
/clone="RHOH1\_41\_B01\_A002"  
/lab\_host="DH10B-T1 phage-resistant E. coli"  
/clone\_lib="Acid- and alkaline-treated roots"  
/note="Organ: Root; Vector: pME18S-PL3; Site 1: XhoI;  
Site 2: XhoI; The library was prepared from polyA+ RNA  
from 8-day-old roots harvested from Btx623 sorghum  
seedlings grown in hydroponic culture. HCl was added to a  
pH of 3.0 to some seedlings, KOH to a pH of 9.0 for  
others. Roots were harvested 3, 12 and 27 hr after  
addition and pooled for RNA preparation. Double-stranded  
cDNA was cloned unidirectionally into different DraIII  
sites of the pME18S-PL3 vector (5-prime DraIII site is  
CAGTGTGTG, 3-prime draIII site is CACCATGTG). XhoI excises  
the cDNA insert."

## ORIGIN

Query Match 44.6%; Score 623.2; DB 7; Length 859;  
Best Local Similarity 81.5%; Pred. No. 6.8e-135;  
Matches 782; Conservative 0; Mismatches 73; Indels 105; Gaps 1;

## RESULT 9

CA213307  
LOCUS  
DEFINITION  
SCQGSB1140A09.g SB1 Saccharum officinarum cDNA clone SCQGSB1140A09  
5', mRNA sequence.  
ACCESSION  
VERSION  
CA213307  
CA213307.1 GI:35259472

```

QY 68 GGGATTAGGGATGGACGGGCGCGGTGGGGAGTTTCAGCGCAGCATACCGCACGGCGG 127
DB 5 GTGAGAGGCATGGACGGAGCTCCGGTCCGCGAGTTTCGGCGACGGTACGCGCAACCG 64
QY 128 CCGGTACCTGCTCTACGACATCTTCGGGAAACAAAGTTTCGAGGTGACCAACAAAGTACAGCC 187
DB 65 CCGGTCTCTGAGTACACATCTTCGGCAACCTGTTTCGAGATCAGCGACAAAGTACAGCC 124
QY 188 GCCCATCATGCCCATTGGCGCGCGCTTACGAGATCGTCTCGTGTGATGAATTTGA 247
DB 125 TCCCATCATGCCCATCGGCGGTGGCGCTTACGAGATCGTCTCGTGTGATGAATTTGA 184
QY 248 GACGAGGAGATGGTGGCGATTAAGAGATCGCCACGCGTTCAACAAAGCATGACGCC 307
DB 185 GACGAGGAGATGGTGGCGATTAAGAGATCGCCACGCGTTTCGACAAACATGAGCC 244
QY 308 CAAGCGCAGCTCCGCGGAGATCAAGCTCTCAGGACCTTCGACGACGAGAAATCATAGG 367
DB 245 CAAGCGCAGCTCCGCGGAGATCAAGCTCTCAGGACCTTCGACGACGAGAAATCATAGG 304
QY 368 CATCAGGATGTGATCCCGCGCGATCCCTCAGGCGTTTCAACGAGCTTACATGCCAC 427
DB 305 CATCAGGAGCTGATCCCGCGCGATCCCGCGCGGTTTCAACGAGCTTACATGCCAC 364
QY 428 GAGAGTCATGACACCGAGCTTCATCATCATCATCTCCGCTCAACCAAGAACTGTGAGAGA 487
DB 365 GAGAGTCATGACACCGAGCTTCATCATCATCATCTCCGCTCAACCAAGAACTGTGAGAGA 384
QY 488 GCACTGCCAGTATTTCTGTACAGATCTGTGGGGGGCTCAAGTACATCATCTCGCGGAA 547
DB 385 ----- 384
QY 548 CGTGATCCACCGGAGCTTGAAGCCGAGCAACCTGCTGTGTAACCCAACTGCGACCTCAA 607
DB 385 -----TCCACCGGAGCTTCAAGCCGAGCAACCTGCTGTGTAACCCAACTGCGACCTCAA 439
QY 608 GATCTCGAGCTTCCGGCTGCGCGCGCTGCTCGGAGGAGCATATGATGCGAGTACGT 667
DB 440 GATCTCGAGCTTCCGGCTGCGCGCGCTTCTCCGAGAGCGCATATGATGCGAGTACGT 499
QY 668 GGTACCCCGGTGTACCGCGCGCGGAGCTGCTCACTCCACGAGTACTCCGCGCG 727
DB 500 GGTGACACGGTGTACCGCGCGCGGAGCTGCTCACTCCACGAGTACTCCGCGCG 559
QY 728 CATCGAGCTCTGCTCGGCTCGGCTGCTCTTTCATGAGCTCATCAACCGCGAGCGCTCTT 787
DB 560 CATCGAGCTCTGCTCGGCTCGGCTGCTCTTTCATGAGCTCATCAACCGCGAGCGCTCTT 619
QY 788 CCGCGGAGGAGCACATGACACAGATGCGCTCATCCGAGGTGATCGGAGCGCGAC 847
DB 620 CCGCGGAGGAGCACATGACACAGATGCGCTCATCCAGAGTGTATCGGAGCGCGAC 679
QY 848 GAGAGGAGCTGGGTTTCATAGGACGAGGAGCGGAGGAGTACATGAGGAGCGCTGCC 907
DB 680 GAGAGGAGCTGGGTTTCATCGGACGAGGAGCGGAGGAGTGTCCCGGAGTGTGAGCGCTCGA 739
QY 908 GCATGATCCCGCGCGGAGCTTCCGCGAGCTGTTCCCGGAGTGTGAGCGCTCGA 967
DB 740 GCATGATCCCGCGCGGAGCTTCCGCGAGCTGTTCCCGGAGTGTGAGCGCTCGA 799
QY 968 CCTCATCGAGAGATGCTCACTTCAACCGCTGCGAGAGTACATGAGGAGGCGCT 1027
DB 800 CCTCATCGAGAGATGCTCACTTCAACCGCTGCGAGAGTACATGAGGAGGCGCT 859

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KEYWORDS      Saccharum officinarum
SOURCE        Saccharum officinarum
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
              clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
              complex.
REFERENCE     1 (bases 1 to 718)
AUTHORS      Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE        The libraries that made SUCEST
JOURNAL      Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT      Contact: Arruda P
              Centro de Biologia Molecular e Engenharia Genetica
              Universidade Estadual de Campinas
              Caixa Postal 6010, 13083-970, Campinas SP, Brazil
              Tel: 55 19 3788 1137
              Fax: 55 19 3788 1089
              Email: parruda@unicamp.br
              Clone distribution: clone distribution information can be found
              through the Brazilian Clone Collection Center (BCCC) at
              http://www.bccceniter.fcav.unesp.br
              Plate: 140 row: A column: 09
              Seq primer: T7 promoter Primer.
              Location/Qualifiers
                1..718
                  /organism="Saccharum officinarum"
                  /mol_type="mRNA"
                  /db_xref="taxon:4547"
                  /clone="SCQSB1140A09"
                  /lab_host="DH10B"
                  /clone_lib="SBI"
                  /notes="Organ: Stalk Bark from adult plants; Vector:
                  pSport1; Site 1: SalI; Site 2: NotI; An unidirectional
                  cDNA library generated from [stalk bark from adult
                  plants]. cDNA was prepared from polyA+ mRNA using
                  SuperScript Plasmid System Kit (Invitrogen). The
                  double-strand cDNAs were fractionated in a sepharose
                  CU-2B 40cm-columns and fragments sizing between 0.8 and
                  1.5 Kb were directionally cloned into the vector. Details
                  of each source of RNA and library construction can be
                  obtained at http://sucest.lad.ic.unicamp.br/public"

ORIGIN
Query Match      43.8%; Score 611.4; DB 6; Length 718;
Best Local Similarity 91.4%; Pred. No. 3.9e-132;
Matches 656; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

QY 107 GCGGAGATGACGACGCGCGCGGTACCTGCTCTAGCATCTTCGGGACAAAGTTCCA 166
DB 1 GCGGAGGTGACGACGCGCGCGGTCTCTGAGTACAAACATCTTCGGCAACCTGTTCGA 60

QY 167 GGTGAGCAACAGTACGACGCGCGCCCATCATGCCCCATTGGCGCGCGCTACGGGATCGT 226
DB 61 GATCAGCACAAGTACCAAGCTCCCATCATGCCCCATCGCGCGCGCTACGGGATCGT 120

QY 227 CTGCTCGGTGATGAACCTTTGAGACGAGGAGATGGTGGCGATTAAGAAGATGCCAACGC 286
DB 121 CTGCTCGGTGATGAACCTTTGAGACGAGAGATGGTGGCCATCAAGAAGATGCCAACGC 180

QY 287 GTTCACACGACATCGACGCGCGCGCGCGCTCGCGGAGATCAAGCTCTCAGGCACCT 346
DB 181 CTTTCGACACCAATGAGCGCGCGCGCGCGCTCGCGGAGATCAAGCTCTGAGGCACCT 240

QY 347 CGACACGAGAAACATCATAGGCATCAGGGATGTGATCCGCGCGCGCTACCGTCAGGCGTT 406
DB 241 CGACACGAGAAACATCATAGGCATCAGGACGTGATCCGCGCGCGCTACCGTCAGGCGTT 300

QY 407 CAAACGAGTCTACATCGCCACGAGCTCATGGACACCGACCTCCATCATCATCCGCTC 466
DB 301 CAAACGAGTCTACATCGGACGAGCTCATGGACACCGACCTCCATCATCATCCGCTC 360

QY 467 CAAACGAGTCTCAGAGAGACCTGCCAGTATTTCTGTACCATCTCGCGGGCT 526
DB 467 CAAACGAGTCTCAGAGAGACCTGCCAGTATTTCTGTACCATCTCGCGGGCT 526

Db 361 CAAACGAGAGCTCTCGGAGGACACTGCCAGTACTTCTGTACCAGATCTCTTGGGGCT 420
QY 527 CAAAGTACATCCACTCGGGAACGATGATCCACCGGACCTGGAAGCCGAGCAACTGCTGCT 586
DB 421 CAAAGTACATCCACTCGGGAACGATGATCCACCGGACCTGGAAGCCGAGCAACTGCTGCT 480
QY 587 GAACGCCAACTCGGACCTCAAGATCTGGGACTTCGGGCTGGCGGCGCTGCTCGGAGAG 646
DB 481 GAACGCCAACTCGGACCTCAAGATCTGGGACTTCGGGCTGGCGGCGCTGCTCGGAGAG 540
QY 647 GCACATGATGACGAGTACGTTGTCACCGGTTGACCGGCGCGGAGCTGCTGCTCAA 706
DB 541 GCACATGATGACGAGTACGTTGTCACCGGTTGACCGGCGCGGAGCTGCTGCTCAA 600
QY 707 CTCCACCGACTACTCCGCGCCATCGAGCTCTGTCGCTCGGCTGCATCTTCATGAGCT 766
DB 601 CTNACCGACTACTTCGCGCATCGAGCTCTGTCGCTCGGCTGCATCTTCATGAGCT 660
QY 767 CATCAACCGCAGCGCGCTCTTCCCGGAGGAGACACATGACAGATGCGCTCAT 823
DB 661 CATCAACCGCAGCGCGCTCTTCCCGGAGGAGACACATGACAGATGCGCTCAT 718

RESULT 10
CK077805 LOCUS
DEFINITION Oryza sativa cv. LYP9 booting whole plant cDNA
            library Oryza sativa (indica cultivar-group) cDNA 5', mRNA
            sequence.
ACCESSION CK077805
VERSION CK077805.1 GI:58689118
KEYWORDS EST.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Euphorbiales; Oryzae; Oryza.
REFERENCE 1 (bases 1 to 632)
AUTHORS Yu,J., Wang,J., Lin,W., Li,S., Li,H., Zhou,J., Ni,P., Dong,W.,
          Hu,S., Zeng,C., Zhang,J., Zhang,Y., Li,R., Xu,Z., Li,S., Li,X.,
          Zheng,H., Cong,L., Lin,L., Yin,J., Geng,J., Li,G., Shi,J., Liu,J.,
          Lv,H., Li,J., Wang,J., Deng,Y., Ran,L., Shi,X., Wang,X., Wu,Q.,
          Li,C., Ren,X., Wang,J., Wang,X., Li,D., Liu,D., Zhang,X., Ji,Z.,
          Zhao,W., Sun,Y., Zhang,Z., Bao,J., Han,Y., Dong,L., Ji,J., Chen,P.,
          Wu,S. and Liu,J.
          The Genomes of Oryza sativa: A History of Duplications
          PLoS Biol. 3 (2), e38 (2005)
          15685232
          Contact: Yan Zhou
          Bioinformatics Department
          Hangzhou Genomics Institute
          No.51 Zhijiang Road, Hangzhou 310008, China
          Tel: 86-571-56805886
          Fax: 86-571-56805884
          Email: zhouyan@genomics.org.cn
          Seq primer: M13 Forward
          High quality sequence stop: 632
          POLYA=No.
          Location/Qualifiers
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              /mol_type="mRNA"
              /cultivar="LYP9"
              /db_xref="taxon:39946"
              /tissue_type="whole plant"
              /dev_stage="booting"
              /clone_lib="Oryza sativa cv. LYP9 booting whole plant cDNA
              library"

ORIGIN
Query Match      43.6%; Score 608; DB 7; Length 632;
Best Local Similarity 99.5%; Pred. No. 2.4e-131;
Matches 621; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
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Clade: Panicoidae; Andropogoneae; Zea.  
 1 (bases 1 to 819)  
 Walbot,V.  
 Maize ESTs from various cDNA libraries sequenced at Stanford  
 University  
 Unpublished (1999)  
 Contact: Walbot V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Plate: 3530.1.21.1 row: C column: 01.

FEATURES  
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 /organism="Zea mays"  
 /mol\_type="mRNA"  
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 /db\_xref="taxon:4577"  
 /tissue\_type="multiple"  
 /dev\_stage="varies by tissue"  
 /lab\_host="DH10B"  
 /clone\_lib="3530 - Full length cDNA library created by  
 Invitrogen from multiple tissues"  
 /notes="Organ: silks, husks, ears, pollen, shoot tips,  
 leaf, root tips, whole seed, embryo; Vector: pCMV-SPORT  
 6.1; Site 1: EcoRV; Site 2: NotI; Maize Gene Discovery  
 Project contracted with Invitrogen to produce a  
 normalized, full length library in a pSPORT vector. This  
 is a Gateway compatible vector, permitting clone movement  
 to new vector backbones for expression in diverse host  
 cells using recombination rather than restriction enzymes.  
 Details of the vector and sequencing primers are available  
 at ZmDB in the EST library description tables. poly(A)+  
 mRNA was prepared by Invitrogen, and equimolar amounts of  
 RNA from each of the 12 tissue samples were mixed together  
 for selection of mRNA with a 5' cap. After synthesis of  
 cDNA, a normalization step was conducted against the  
 mixture of RNA sources. This step effected a 20X to 80X  
 reduction in common transcript types. Tissues prepared: 1.  
 Just emerging silks; 2. Inner husks from ears of sample  
 #1; 3. 20 day aleurone; 4. Immature tassels, stages from  
 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm  
 vegetative shoot tips from 15 day old seedlings; all  
 leaves with an expanded or partially expanded sheath  
 were removed; 8. mature leaf tissue; 9. 0.5 cm long root  
 tips from 15 day old seedlings; 10. 10 day whole seed; 11.  
 12 day endosperm and embryo; 12. 17 day endosperm and  
 embryo. All of the sequenced clones in project 3530 will  
 be archived at the University of Arizona along with the  
 Unigene clones from the Maize Gene Discovery EST  
 sequencing projects. Clones can be ordered through the  
 ZmDB web site or directly from the University of Arizona  
 (<http://www.genome.arizona.edu/orders/>). High density  
 filters containing over 18,000 clones can also be ordered  
 from the University of Arizona."

ORIGIN  
 Query Match 43.3%; Score 603.8; DB 6; Length 819;  
 Best Local Similarity 88.7%; Pred. No. 2.4e-130;  
 Matches 653; Conservative 0; Mismatches 83; Indels 0; Gaps 0;  
 QY 48 GCGCCGAGAGAGGAGGAGGATAGGAGTACGGCGCGCGCGCGGAGTTTCAGG 107  
 Db 84 GCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 143  
 QY 108 CCGACGATACGACGCGCGCGCGGAGTACCTCTACGACATCTTCGGGAAACAGTTTCGAG 167  
 Db 144 CAGACGGTGACGACGCGCGCGCGGTTCTCTGCAGTACACATCTTCGGCAACCTGTTTCGAG 203  
 QY 168 GTGACGAACAGTACACGCGCGCGCGCCATCATGCCATTCGGCGCGCGCGCTACGGGATCGTC 227

Db 204 ATCAGCACAAGTACACAGCCCCCCCCCATCATGCCCATTCGGCCGCGCGCGCTACGGGATCGTC 263  
 QY 228 TGCTCCGCTGATGAACCTTTTGAGACGACGAGGAGATGGTGGCGATAAAGAAGATCCGCCAACGCG 287  
 Db 264 TGCTCGGTGATGACTCCGAGACGAGGAGGATGGTGGCCATCAAGAGATCCGCCAACGCG 323  
 QY 288 TTCAACAACGACATCGACGCCCAAGCGCAGCTCCGGGAGATCAAGCTCTCTCAGGACACCTC 347  
 Db 324 TTGCAACAACCATGGACGCCCAAGCGCAGCTCCGGGAGATCAAGCTCTCAGGACACCTC 383  
 QY 348 GACCAAGAGAACATCATAGGATCAGGATGTGATCCGCCGCCGATCCCTCAGGCGTTTC 407  
 Db 384 GACCAAGAGAACATCATAGGATCAGGATGTGATCCGCCGCCGATCCCTCAGGCGTTTC 443  
 QY 408 AACGACGCTCTACATCGCCACGCGAGCTCATGGACACGACCTCCATCACATCATTCGGCTCC 467  
 Db 444 AACGACGCTGTATCATCGGACGCGAGCTGATGACACGACCTCCACACATCATTCGGTCC 503  
 QY 468 AACCAAGAACTGTTCAGAAAGACACTGCCAGATATTTCTGTATCCAGATCTTCGGGGGCTC 527  
 Db 504 AACCAAGGAGCTCTCGGAGGAGCACTCCAGTACTTTCATGTATCCAGATCTTCGGGGGCTC 563  
 QY 528 AAGTATATCCACTCCGGCGAAAGTGTATCCACCGGACCTGAAGCCGAGCAACCTGCTGCTG 587  
 Db 564 AAGTATATCCACTCCGGCGAAAGTGTATCCACCGGACCTGAAGCCGAGCAACCTGCTGCTG 623  
 QY 588 AACGCAAACTGCGACCTCAAGATCTGCACTTCGGGCTGGCGCGCGCTGCTGCTGCGAGAGC 647  
 Db 624 AACGCAAACTGCGACCTCAAGATCTGCACTTCGGGCTGGCGCGCGCTGCTGCTGCGAGAGC 683  
 QY 648 GACATGATGACGAGTACGTGTCAACCGGTGTACCCGCGCGCGAGCTGCTGCTCAAC 707  
 Db 684 GACATGATGACGAGTACGTGTCAACCGGTGTACCCGCGCGCGAGCTGCTGCTCAAC 743  
 QY 708 TCACCGGACTACTCCGCGCGCATCGAGTCTGGTCTGGTCTGGTCTGGTCTGGTCTGGTCTGG 767  
 Db 744 TCACCGGACTACTCCGCGCGCATCGAGTCTGGTCTGGTCTGGTCTGGTCTGGTCTGGTCTGG 803  
 QY 768 ATCAACCGCGCGCGCGC 783  
 Db 804 ATCAACCGCGCGCGCGC 819

RESULT 13  
 AL504341  
 LOCUS AL504341 700 bp mRNA linear EST 04-JAN-2001  
 DEFINITION AL504341 Hordeum vulgare Barke roots Hordeum vulgare subsp. vulgare  
 CDNA clone HW04P17V 5', mRNA sequence.  
 ACCESSION AL504341  
 VERSION AL504341.1 GI:12030556  
 KEYWORDS EST.  
 SOURCE Hordeum vulgare subsp. vulgare  
 ORGANISM Hordeum vulgare subsp. vulgare  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Poideae; Triticeae; Hordeum.  
 REFERENCE 1 (bases 1 to 700)  
 AUTHORS Michalek,W., Weschke,W., Pleissner,K.-P. and Graner,A.  
 EST sequencing and analysis in barley  
 TITLE Unpublished (2000)  
 JOURNAL Contact: Michalek W  
 COMMENT Institute for Plant Genetics and Crop Plant Research  
 Corrensstr.3, D-06466 Gatersleben, Germany  
 Email: michalek@ipk-gatersleben.de, <http://pgrc.ipk-gatersleben.de>  
 Seq primer: f3 primer for 5'end.  
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 1..700  
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 /mol\_type="mRNA"  
 /cultivar="Barke"  
 /sub\_species="vulgare"  
 /db\_xref="taxon:112509"  
 /clone="HW04P17V"



Db	478	AGATCCCGTCTATACCTGCTTTGTACATATGATCAAGATTGAGACGCCGGTACACTGAAC	537
Qy	1268	ATTGCAATTTGTTTGTGTTGATGTTTCGAAACCCACATTCCTGCAAGTTGTGGCTGCTT	1327
Db	538	-TTGCATTTGTTTGTGTTGATGTTTCGAAACCCACATTCCTGCAAGTTGTGGCTGCTT	596
Qy	1328	TGTATGATATATGTTACTATGTTTCGAATAAAAGGGTTTGGAACTTTTGGATTAAAAAAA	1387
Db	597	TGTATGATATATGTTACTATGTTTCGAATAAAAGGGTTTGGAACTTTTGGATTATGATATAAA	656
Qy	1388	AAAAAAAAAA 1396	
Db	657	AAAAAAAAAA 665	

RESULT 15  
CF985761  
LOCUS  
DEFINITION  
238068base.4369.y1 Oryza sativa cv. LYP9 tillering whole plant  
cDNA library Oryza sativa (indica cultivar-group) cDNA 5', mRNA  
sequence.

ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
CF985761	CF985761.1	GI:58587453	EST.	
			<i>Oryza sativa</i> (indica cultivar-group)	
			<i>Oryza sativa</i> (indica cultivar-group)	
			Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzoae; Oryza.	

REFERENCE  
AUTHORS

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Yu, J., Wang J., Lin, W., Li, S., Li, H., Zhou, J., Ni, P., Dong, W.,  
Hu, S., Zeng, C., Zhang, J., Zhang, Y., Li, R., Xu, Z., Shi, S., Li, X.,  
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Li, C., Ren, X., Wang, J., Deng, X., Li, D., Liu, D., Zhang, X., Ji, Z.,  
Zhao, W., Sun, Y., Zhang, Z., Bao, J., Han, Y., Dong, L., Ji, J., Chen, P.,  
Wu, S. and Liu, Y.

**TITLE**  
The Genomes of *Oryza sativa*: A History of Duplications  
**JOURNAL**  
PLOS Biol. 3 (2), e38 (2005)

15685292  
Contact: Yan Zhou  
Bioinformatics Department  
Hangzhou Genomics Institute  
No.51 Zhijiang Road, Hangzhou 310008, China  
Tel: 86-571-56805886  
Fax: 86-571-56805884  
Email: zhouyan@genomics.org.cn  
Seq primer: M13 Forward  
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## ALIGNMENTS

## RESULT 1

ADT02329

ID ADT02329 standard; cDNA; 1396 BP.

XX ADT02329;

DT 13-JAN-2005 (first entry)

DE Rice mitogen-activated protein kinase 5a (MAPK5a) cDNA.

XX Rice; mitogen-activated protein kinase 5a; MAPK5; MAPK5a; gene; ss;  
XX abiotic stress tolerance; biotic stress tolerance; drought; temperature;  
XX salinity; plant.

OS Oryza sativa.

XX Key Location/Qualifiers

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XX 21-OCT-2004.

XX 31-JAN-2004; 2004US-00768886.

XX 31-JAN-2003; 2003US-0444249P.

XX (YANG/) YANG Y.

XX (XIONG/) XIONG L.

XX Yang Y, Xiong L;

XX WPI; 2004-747214/73.

XX P-PSDB; ADT02330.

XX GENBANK; AF479883.

XX New isolated nucleic acid molecule encoding a mitogen-activated protein kinase-5 (MAPK5) polypeptide, useful for increasing tolerance to abiotic and biotic stress in plants.



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QY	108	CCGACGATGACGACCGCGCGCGGTACTGCTCTACGACATCTTCGGGAACAAGTTTCGAG	167
DB	148	CAGACGCTGACGACCGCGCGCGGTTCCTGCAGTCAACATATTCCGCAACCTGTTTCGAG	207
QY	168	GTGACGACAGATACGACCGCGCGCGCCATGCCCCATTTGGCGCGCGCGCTACGGGATCGTC	227
DB	208	ATCAGCGACAGATACGACCGCGCGCGCCATGCCCCATTCGCGCGCGCGCTACGGGATCGTC	267
QY	228	TGCTCCGTGATGAATTTGAGAGAGAGAGATGGTGGCGATMAAGAGATCGCCACGCG	287
DB	268	TGCTCTGTGATGAATCTCCGAGAGAGAGATGGTGGCCATCAAGAGATCGCCACGCG	327
QY	288	TTCAAACAAGACATGACGCGCAAGCGCACGCTCCGGAGATCAAGTCTCTCAGGCACTTC	347
DB	328	TTCCGACAAACCAATGACGCGCAAGCGCACGCTCCGGAGATCAAGTCTCTCAGGCACTTC	387
QY	348	GACCAAGAGACATCATAGGACATCAGGATGTGATCCCGCGCGCGATCCCTCAGGCGTTC	407
DB	388	GACCAAGAGACATCATAGGACATCAGGATGTGATCCCGCGCGCGATCCCTCAGGCGTTC	447
QY	408	AACGAGCTCTACATCGCAGGAGCTCATGACACGAGACCTCCATCACAATCATCCGCTCC	467
DB	448	AACGAGCTCTACATCGCAGGAGCTCATGACACGAGACCTCCATCACAATCATCCGCTCC	507
QY	468	AACCAAGAACTGTGAGAGACACTGCCAGATTTCTCTGACAGATCTTCGGCGGGGCTC	527
DB	508	AACCAAGAACTGTGAGAGACACTGCCAGATTTCTCTGACAGATCTTCGGCGGGGCTC	567
QY	528	AGTACATCACTCGCGAGAGCTGATCCACCGGAGCTGAGCGGAGCAACCTGCTGCTG	587

Db	568	AGTACATCCACTCCGCGCAACGTGATCCACCGTGAACCTCAAGCCGAGCAACCTGCTGCTG	627
QY	588	AACGCAAACTGCGACCTCAAGATCTGCGACTTTCGGGCTGGCGCGCGCTGCTCGGAGAGC	647
DB	628	AAGCCAACTGCGACCTCAAGATCTGCGACTTTCGGGCTGGCGCGCGCTGCTCGGAGAGC	687
QY	648	GACATGATGACGAGTACGTGTGTCACCGGTGTTACCGGCGCGCGAGTGTGCTCAAC	707
DB	688	GACATGATGACGAGTACGTGTGTCACCGGTGTTACCGGCGCGCGAGTGTGCTCAAC	747
QY	708	TCCACCGGACTACTCCGCGCCATCGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	767
DB	748	TCCACCGGACTACTCCGCGCCATCGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	807
QY	768	ATCAACCGCGCGCGCTCTTCCCGCGAGGACCAACATGACCATGCGCTCATCAC	827
DB	808	ATCAACCGCGCGCGCTCTTCCCGCGAGGACCAACATGACCATGCGCTCATCAC	867
QY	828	GAGGTGATCGGAGCGCGCGAGCGAGCTGGGTTTCATACGGAACGAGACCGGAGG	887
DB	868	GAGGTGATCGGAGCGCGCGAGCGAGCTGGGTTTCATACGGAACGAGACCGGAGG	927
QY	888	AGTACATGAGGACCTGCGCGAGTACCGCGCGCGAGCTTCGCGAGCATGTTCCCGCG	947
DB	928	AGTACATGAGGACCTGCGCGAGTACCGCGCGCGAGCTTCGCGAGCATGTTCCCGCG	987
QY	948	GTGACGCGCGCGCGCTCGACCTCATCGAGAGGATGCTCACCTTCAACCGCGCTGCAGAG	1007
DB	988	ATGACGCGCGCGCTCGACCTCATCGAGAGGATGCTCACCTTCAACCGCGCTGCAGAG	1047
QY	1008	ATCAGATGAGGAGCGCGCTCGATCATCTTACCTAGAGAGATTGCAAGATCGCGAT	1067
DB	1048	ATCAGATGAGGAGCGCGCTCGATCATCTTACCTAGAGAGATTGCAAGATCGCGAT	1107
QY	1068	GAGCCCATCTGCTGAGCGCTTCTCTTCCGCTTTCGAGTTCGAGCAGAGGCTTAAACGAGG	1127
DB	1108	GAGCCCATCTGCTGAGCGCTTCTCTTCCGCTTTCGAGTTCGAGCAGAGGCTTAAACGAGG	1167
QY	1128	CAAAATGAAGCAGCTGATCTTCAACGAAGCGATCGAGATGAACCAACATCTCGGTACTAG	1187
DB	1168	CAAAATGAAGCAGCTGATCTTCAACGAAGCGATCGAGATGAACCAACATCTCGGTACTAG	1227
QY	1188	ATTG 1191	
DB	1228	CTAG 1231	
RESULT 3			
ID	AAC84259	standard; cDNA; 1125 BP.	
XX	AAC84259;		
AC	AAC84259;		
DT	19-MAR-2001	(first entry)	
XX			
DE	Signal transduction protein encoding cDNA.		
XX			
KW	Zea mays; maize; signal transduction protein; phytohormone; ethylene;		
KW	auxin; cytokinin; gibberellin; immunogen; ss.		
XX			
OS	Zea mays.		
XX			
FT	Key	Location/Qualifiers	
FT	CDS	1..1125	
FT	/tag=	a	
XX	/product=	"signal transduction protein"	
PN	WO200070059-A2.		
XX			
PD	23-NOV-2000.		
XX			
PP	28-APR-2000; 2000WO-US011687.		
XX			

PR 14-MAY-1999; 99US-0134292P.  
 PR 08-JUL-1999; 99US-0142996P.  
 XX (PION-) PIONEER HI-BRED INT INC.  
 PA Helentjaris TG;  
 XX  
 PI  
 XX  
 XX WPI; 2001-031929/04.  
 DR P-PSDB; AAB48046.  
 XX  
 XX New signal transduction nucleic acids and encoded proteins useful for  
 PT regulating phytohormone expression, including ethylene, auxins,  
 PT cytokinins and gibberellin, to provide control of plant response to  
 PT environmental stresses.  
 XX  
 PS Claim 1; Page 89-90; 126pp; English.  
 CC The invention provides Zea mays signal transduction proteins and encoding  
 CC nucleotide sequences. The nucleic acids are useful for regulating  
 CC expression of phytohormones, including ethylene, auxins, cytokinins, and  
 CC gibberellin, to effect developmental changes in plants and provide  
 CC control of plant response to environmental stresses. They may also be  
 CC used as probes or amplification primers in the detection, quantitation or  
 CC isolation of gene transcripts, for detecting mutations in the gene, for  
 CC monitoring upregulation of expression or changes in enzyme activity in  
 CC screening assays of compounds, for detection of any number of allelic  
 CC variants, or for site-directed mutagenesis in eukaryotic cells. They may  
 CC further be used for recombinant expression of their encoded polypeptides,  
 CC as immunogens in the preparation or screening of antibodies, and in sense  
 CC or antisense suppression of genes in a host cell, tissue or plant. The  
 CC proteins may be used in assays for enzyme agonists or antagonists, as  
 CC immunogens or antigens to obtain antibodies specifically immunoreactive  
 CC with the proteins. The present sequence represents a cDNA encoding a  
 CC signal transduction protein of the invention  
 XX  
 SQ Sequence 1125 BP; 241 A; 390 C; 317 G; 177 T; 0 U; 0 Other;  
 Query Match 65.6%; Score 915.8; DB 4; Length 1125;  
 Best Local Similarity 88.7%; Pred. No. 1.3e-178;  
 Matches 992; Conservative 0; Mismatches 127; Indels 0; Gaps 0;  
 QY 69 GGATTAGGATGACGGGGCGCGGTGGCGGAGTTTCAGGCGCGAGTACGACGCGCGC 128  
 DB 7 GGAGAGCGGTGACGCGAGTCCGGTCCGCGAGTTCGGGAGCGGTGACGCGCGCGC 66  
 QY 129 CGGTACCTGCTTACGACATCTTCGGGAACAAGTTTCAGGTGACGAAACAAGTACCGCG 188  
 DB 67 CGGTCTTCAGTACATCTTCGGCAACTGTTCCGAGATCAGGCAAGTACCGCGC 126  
 QY 189 CCATCATGCTTGGCGCGCGCGCTTACGGGATCGTCTGCTCCGTGATGAATTTGAG 248  
 DB 127 CCATCATGCTTGGCGCGCGCGCTTACGGGATCGTCTGCTCCGTGATGAATTTGAG 186  
 QY 249 ACGAGGAGATGTTGGCGATTAAGAAGTACGCAACGCGTTTCAACACGACATGAGCGC 308  
 DB 187 ACGAAGGAGATGTTGGCGATTAAGAAGTACGCAACGCGTTTCAACACGACATGAGCGC 246  
 QY 309 AAGCGCACGCTCCGGGAGATCAAGCTCTCAGGCACCTCCGACCAACGAGAACATCATAGGC 368  
 DB 247 AAGCGCACGCTCCGGGAGATCAAGCTCTCAGGCACCTCCGACCAACGAGAACATCATAGGC 306  
 QY 369 ATCAGGATGTGATCCCGCGCGCGATCCCTCAGCGGTTCAACGACGCTTACATCGCCACG 428  
 DB 307 ATCAGGACGATGATCCCGCGCGCGATCCCTCAGCGGTTCAACGACGCTTACATCGCCACG 366  
 QY 429 GAGCTCATGACACCGGACCTCCATCATATCGCTTCAACGACGCTTCAAGAGAG 488  
 DB 367 GAGCTCATGACACCGGACCTCCATCATATCGCTTCAACGACGCTTCAAGAGAG 426  
 QY 489 CACTGCGAGTATTTCTGTATCAGATCCTCGCGGGGCTCAAGTATCATCTCCGCGGAAC 548  
 DB 427 CACTCCAGTACTTTCATGTACCATCTCTCGCGGGGCTCAAGTATCATCTCCGCGGAAC 486

QY 549 GTGATCCACCGCGAGCTGAAGCGGAGCAACCTGTCTGAAAGCGCCAACTCGGACCTCAAG 608  
 DB 487 GTGATCCACCGCGAGCTGAAGCGGAGCAACCTGTCTGAAAGCGCCAACTCGGACCTCAAG 546  
 QY 609 ATCTGCGACTTCGGGCTGGCGGGCGTCTCGGAGAGCGACATGATGACGAGTACGTG 668  
 DB 547 ATCTGCGACTTCGGGCTGGCGGGCGTCTCGGAGAGCGACATGATGACGAGTACGTG 606  
 QY 669 GTACCCCGGTGTACCGCGCGCGGAGCTGCTCAACTCCACCGACTACTCCGCGGCC 728  
 DB 607 GTACCGCGGTGTACCGCGCGCGGAGCTGCTCAACTCCACCGACTACTCCGCGGCC 666  
 QY 729 ATCGAGCTGTGCTCGGCTGGCTGCTCTTCATGAGAGCTCATCAACCGCGAGCGCTCTTC 788  
 DB 667 ATCGAGCTGTGCTCGGCTGGCTGCTCTTCATGAGAGCTCATCAACCGCGAGCGCTCTTC 726  
 QY 789 CCGGCGAGGACCAATGACCAAGATGCGCTCTCATCCAGAGTGTATCGGAGCGCGGACG 848  
 DB 727 CCGGCGAGGACCAATGACCAAGATGCGCTCTCATCAACCGAGGTGATCGGAGCGCGGACG 786  
 QY 849 GACGAGAGCTGGGTTTCATGCGAAGAGGAGCGGAGGAGTACATGAGGACCTGCGCG 908  
 DB 787 GACGATGAGCTGGGTTTCATGCGAAGAGGAGCGGCGGAGTACATGCGGACCTGCGCG 846  
 QY 909 CAGTACCCCGCGCGGAGCTTCGCGAGCATGTTCCCGCGGTCGAGCGCGCGCTCGAC 968  
 DB 847 CAGTTCCTCCCGCGCGGCGGCTGTCGACCTGTTCCCGGAGTACGCGCGCTCGGCGTGGAC 906  
 QY 969 CTCTATCGAGAGGATGCTCACTTTCAACCGCTGCGAGAGTACACAGTTGAGGAGGCGCTC 1028  
 DB 907 CTCTATCGAGGAGTGTCTCACTTTCAACCGCTGCGAGAGTACACAGTTGAGGAGGCGCTG 966  
 QY 1029 GATCATCTTACCTGAGAGATGTCAGCATCGCGAGTACGCGGATCTGCTGAGGCGCC 1088  
 DB 967 GAGCACCGCTTACCTGGAAGGCTTACACGAGCTGCGCGAGCGAGCCATCTGACGAGCCG 1026  
 QY 1089 TTCTCTCTGACTTCGAGCAGAGGCTCTAAACGAGGAGCCAAATGAAGCAGCTGATCTTC 1148  
 DB 1027 TTCTCTGACTTCGAGCAGAGGCTCTGAGCGAAGACCAATGAAGCAGCTGATCTTC 1086  
 QY 1149 AACGAAGCAGTACGAGATGAACCCAAACATCCCGTACTAG 1187  
 DB 1087 AACGAGGCCATGAAGTCAACCCCACTTCGAGTACTAG 1125  
 RESULT 4  
 ADT02331  
 ID ADT02331 standard; cDNA; 1084 BP.  
 XX AC ADT02331;  
 XX DT 13-JAN-2005 (first entry)  
 XX DE Rice mitogen-activated protein kinase 5b (MAPK5b) cDNA.  
 XX KW Rice; mitogen-activated protein kinase 5b; MAPK5; MAPK5b; gene; ss;  
 XX KM abiotic stress tolerance; biotic stress tolerance; drought; temperature;  
 XX KW salinity; plant.  
 XX OS Oryza sativa.  
 XX FH Key Location/Qualifiers  
 XX CDS 78..875  
 XX FT /\*tag= a  
 XX FT /product= "Rice MAPK5b"  
 XX FT /transl\_except= (pos:1..6, aa:Met-Met-Asp)  
 XX PN US2004209325-A1.  
 XX PD 21-OCT-2004.  
 XX PP 31-JAN-2004; 2004US-0076886.  
 XX



functional in a plant cell operably joined to a polynucleotide encoding a polypeptide associated with the property, and growing the transformed plant. The property is selected from improving plant cold tolerance, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for improving plant drought tolerance, for providing increased resistance to plant disease, for galactomannan production, for production of plant growth regulators, for improving plant heat tolerance, for improving plant tolerance to herbicides, for increasing the rate of homologous recombination in plants, for lignin production, for improving plant tolerance to extreme osmotic conditions, for improving plant tolerance to pathogens or pests, for yield improvement by modification of photosynthesis, for modifying seed oil yield and/or content, for modifying seed protein yield and/or content, for yield improvement by modification of carbohydrate, nitrogen or phosphorus use and/or uptake and for yield improvement by providing improved plant growth and development under at least one stress condition. The polynucleotide may also encode a plant transcription factor. The methods and compositions of the present invention are useful in the field of biochemistry and genetics, in particular for producing transgenic plants with improved biological characteristics such as increased yield, improved nitrogen flow, increasing plant tolerance to cold or heat, improving plant tolerance to extreme osmotic and drought conditions, and improving plant tolerance to plant pests or pathogens. They can also be used in physical arrays of molecules, plant breeding markers, computer-based storage and analysis systems. The present sequence is one of the 5544 plant cDNA sequences of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at [seqdata.uspto.gov/sequence.html?DocID=20040216190](http://seqdata.uspto.gov/sequence.html?DocID=20040216190).

Sequence 1837 BP; 393 A; 594 C; 477 G; 373 T; 0 U; 0 Other;

Query Match 44.6%; Score 623.2; DB 13; Length 1837;

Best Local Similarity 70.9%; Pred. No. 2.1e-118;

Matches 892; Conservative 0; Mismatches 343; Indels 23; Gaps 4;

QY	53	GAGAGAGAGGAGGAGGATAGGATGGAGCGGGCGCGCGGAGTTCCAGGCGGAC	112
DB	373	GAGAGTTTCGTGGCGCGTGTGAGATGGAGCGCGCTCGGGTGGCGGCGGAC	432
QY	113	GATGACGACGCGCGCGCGTCTCTACGACATCTTCGGGAAACAAGTTCCAGGTTGAC	172
DB	433	GATGACGACGCGCGCGCGTCTCTCTACACATATTCGGCAACAGTTCCAGATCAC	492
QY	173	GAAACAAGTACAGCGCCCAATATGCCCCATTGGCGCGCGCTTACGGGATCTGTGCTC	232
DB	493	GGCCAAAGTACAGCGCGCGCATGCCCCATCGCGCGCGCGCTTACGGGATCTGTGCTC	552
QY	233	CGTGATCACTTTGAGACGAGGAGATGGTGGGATAGAGATGCCCAACGGTTCAA	292
DB	553	GGTGATGAATCTTGAGACGAGGAGATGGTGGCAATCAGAAGATGCCAAGCTTTCGA	612
QY	293	CAACGACATCGACGCCAAGCGCAGCTCCGGGAGATCAAGCTCTCAGGACCTCGACCA	352
DB	613	CAACACATCGACGCCAAGCGCAGCTCCGGGAGATCAAGCTCTGAGGACCTCGACCA	672
QY	353	CGAGAACATCATAGGCATCAGGGATGTGATCCCGCGCGCGATCCCTCAGCGGTTCAACGA	412
DB	673	CGAGAACATAGTAGGCTCCGAGATGTGATCCCGCGCGCGATCCCTCAGCGGTTCAACGA	732
QY	413	CGTCTACATCGCACGGAGCTCATGGACACGGACCTTCATCATCATCGCTCCACCA	472
DB	733	CGTCTACATCGCACCGAGCTCATGGACACGGACCTTCATCATCATCGCTCCACCA	792
QY	473	AGAACTGTCAAGAGCAGCTGCCAGTATTTCTGTACAGATCTCTGGGGGGGTCTCAAGTA	532
DB	793	AGCGCTCTCGAAGAACACTGCCAGTACTTCTGGGGCCCGGGCGCGGAGCGGAGCA	852
QY	533	CATCCATCGCGCGAACGTGTATCCACCGCGACCTGGAAGCGGAGCAACCTGTGCTGAACGC	592
DB	853	CATCTCACGGCACTCTGTGCGCGCGCACCGAGGTCTGTCGCGGAGCTGCATCTTTCATGC	912
QY	593	CAACTCGGACCTCAAGATCTGCGGACTTCGGGCTGGCGCGCGCTGTCGGAGAGCGACAT	652

DB	913	CGCCCATCAACCGCGCTCTCTCCCGGGGAGGACACATGACACAGATGCCCGCTAT	972
QY	653	GATGACGAGTACGTGGTCAACCGGTGGTACCGCGC-----GCCGAGCTGTGTC	702
DB	973	GCACGGGGTGTATCTGCACCCCGCGGACAGACAGACCCCGATTCAACCGGACGAGGAC	1032
QY	703	TCAACTCCACCGACTACTTCGGCGCCATCGACGTCTGGTCCGTCGGCTGCATCTTCATGG	762
DB	1033	GCAGAGGTATCATGAGGACCTTCCCGCGGCA--GGGACCAATGACACAGATGGCGCT	1092
QY	763	AGTCTCATCAACCGCGCTCTTCCCGGCA--GGGACCAATGACACAGATGGCGCT	820
DB	1093	CCCCAGGTGCAGCGCGCGCTGGCACTCATCGAGAGGATATTCACCTGATCGGCT	1152
QY	821	CATCACCGAGGTATCGGACCGCGGACGACGACGAGCTGGGGTTTATACGGAACGAGGA	880
DB	1153	TATCAGGATGTATCGGACCGCGGACCGGACCGGACCTGGGTATTAATCGGAACGAGGA	1212
QY	881	CGCGAGGAGTACATGAGG--CACTGCGCGAGTACCGCGCGGAGCTTCCGCGAGCATGT	939
DB	1213	CGCGAGGAGTACATGAGGCGCACCTGCCGAGTTCCCTCGCGGTCTTCCCGGAGCAT	1272
QY	940	TCCCGCGGTGCAGCGCGCGCTCGACTCATCGAGAGGATGCTCACCTTCAACCCCGC	999
DB	1273	TCCCGAGGTGCAGCGCGCGCTGGACTCATCGAGAGGATGCTCACCTTCAACCCCGC	1332
QY	1000	TGCGAGAAATCAAGTTGAGGAGGCGCTCGATCATCTTACCTAGAGAGATTCGACGACA	1059
DB	1333	TGCGAGGATCAAGTTGAGGAGGCGCTCGATCATCTTACCTAGAGAGATTCGACGACA	1392
QY	1060	TGCGGATGAGCCCATCTGCTGGAGCGCTTCTCTTCCGACTTCGAGCAGAGGCTCTAA	1119
DB	1393	TGCGGATGAGCCCATCTGCTGGAGCGCTTCTCTTCCGACTTCGAGCAGAGGCTCTAA	1452
QY	1120	ACGAGGACCAATGAGGAGCTGATCTTCAACGAGGAGTTCGAGATGAAACCAACATCC	1179
DB	1453	CGGAGACCATGAGGAGCTGATCTTCAACGAGGAGTTCGAGATGAAACCAACATCC	1512
QY	1180	GGTACTAGA-----TTGAATCACCATGGAATAGATCCCTCTATATCTGCTTT	1229
DB	1513	GATACTAGAGGATTCATCTCTAGTTACCCCAATAGTATGATTTGATGTAAACTGTTTG	1572
QY	1230	GTACATATGATCAGATTGAGAGCGCGGTAGACTGAACATTGCAATTTGTTGTTGTT	1287
DB	1573	TAATAGGAGTAGGTCAAAGAACATGGTAGATTGCGCACATGCAATTTGTTGTTGTT	1630

RESULT 6

AD084444

ID AD084444 standard; cDNA; 873 BP.

XX

AC AD084444;

XX

DT 21-APR-2005 (first entry)

XX

DE Plant full length insert polynucleotide seqid 3164.

XX

KW plant protectant; plant growth regulator; gene therapy; plant;  
 KW recombinant DNA construct; physical array; plant breeding marker;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
 KW growth rate; cell cycle pathway; disease resistance;  
 KW galactomannan production; lignin production; plant growth regulator;  
 KW yield; plant growth; plant development; seed oil; protein yield;  
 KW protein content; gene; ss.

XX Unidentified.

OS US2004034888-A1.

PN 19-FEB-2004.

PD

28-APR-2003; 2003US-00425114.  
 06-MAY-1999; 99US-00304517.  
 05-NOV-2001; 2001US-00985678.  
 (LIUJ/) LIU J.  
 (ZHOU/) ZHOU Y.  
 (KOVA/) KOVALIC D K.  
 (SCRE/) SCREEN S E.  
 (TABA/) TABASKA J E.  
 (CAOY/) CAO Y.  
 Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
 WPI; 2004-180133/17.  
 New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for improving yield.  
 Claim 1; SEQ ID NO 3164; 15pp; English.  
 The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert polynucleotide that can be used in the recombinant DNA construct of the invention.  
 Sequence 873 BP; 181 A; 277 C; 237 G; 178 T; 0 U; 0 Other;  
 Query Match 38.9%; Score 543; DB 13; Length 873;  
 Best Local Similarity 89.3%; Pred. No. 5.8e-102;  
 Matches 585; Conservative 0; Mismatches 70; Indels 0; Gaps 0;  
 537 CACTCGGCGAAGCTGATCCACCGGACCTGAAGCCGAGCAACCTGCTGTGAACGCCAAC 596  
 1 CACTCGGCGAAGCTGATCCACCGGACCTGAAGCCGAGCAACCTGCTGTGAACGCCAAC 60  
 597 TGGGACCTCAAGATCTCGGACTTCGGGCTGGCGGCGGCGGCTGCTCGGAGAGCGACATGATG 656  
 61 TGGGACCTCAAGATCTCGGACTTCGGGCTGGCGGCGGCGGCTGCTCGGAGAGCGACATGATG 120  
 657 ACGGAGTACGTGTGTACCGGCTGGTGTACCGGCGGCGGAGCTGTGTCTCAACTCCACCGAC 716  
 121 ACGGAGTACGTGTGTACCGGCTGGTGTACCGGCGGCGGAGCTGTGTCTCAACTCCACCGAC 180  
 717 TACTCCGCGCGCCATCGACGCTGT 776  
 181 TACTCCGCGCGCCATCGACGCTGT 240  
 777 CAGCGGCTTTCGCGGCGGAGGACCATGACGACGATGCGGCTGTGTGTGTGTGTGTGTGTGTGT 836  
 241 CAGCGGCTTTCGCGGCGGAGGACCATGACGACGATGCGGCTGTGTGTGTGTGTGTGTGTGTGT 300  
 837 GGGACGCGGACGAGCAGGCTGGGTTTCATACGGAACGAGGACGCGAGGAGGAGTACATG 896  
 301 GGGACGCGGACGAGCAGGCTGGGTTTCATACGGAACGAGGACGCGGAGGAGGAGTACATG 360  
 897 AGGCACCTGCGCGAGTACCGCGCGGACGCTTCCGCGAGCATGTGTCCGCGGGGTGACGCC 956

361 CGCCACCTCCGCGAGTTCGCGCGCGCGGCTTTCGTCAGCCTGTTCCCGGATGCGAGCC 420  
 957 GCGCGCTCGACCTCATCGAGGAGTGTCACTTCAACCGCTCGAGAGATCACAGTT 1016  
 421 GTGCGCTGAGACCTCATCGAGGAGTGTCACTTCAACCGCTCGAGAGATCACAGTT 480  
 1017 GAGGAGGCGCTCGATCATCTTACCTAGAGAGATTGACGACATCCCGGATGAGCCCATC 1076  
 481 GAAAGAGGCGCTGGAGCACCGGTACCTGGAACGGCTACACGAGCTGCGCGAGGCCCATC 540  
 1077 TGCCTGAGGCGCTTCTCTTCTGAGCTTCGAGAGAGAGGTCTTAAACGAGGACCAATGAG 1136  
 541 TGCACGAGCGCGCTTCTCTGAGCTTCGAGAGAGAGGTCTTACGAGGAGACCAATGAG 600  
 1137 CAGCTGATCTTCAACGAGGAGTTCGAGATGAACCCAAACATCCGCTACTAGATTG 1191  
 601 CAGCTGATTTCAACGAGGAGTTCGAGATGAACCCAAACATCCGCTACTAGATTG 655  
 RESULT 7  
 AAC84265  
 ID AAC84265 standard; cDNA; 1197 BP.  
 AC AAC84265;  
 DT 19-MAR-2001 (first entry)  
 DE Signal transduction protein encoding cDNA.  
 KW Zea mays; maize; signal transduction protein; phytohormone; ethylene;  
 KW auxin; cytokinin; gibberellin; immunogen; ss.  
 OS Zea mays.  
 FH Key Location/Qualifiers  
 CDS 1..1197  
 FT /\*tag= a  
 FT /product= "signal transduction protein"  
 XX WO200070059-A2.  
 XX 23-NOV-2000.  
 XX 28-APR-2000; 2000WO-US011687.  
 XX 14-MAY-1999; 99US-0134292P.  
 XX 08-JUL-1999; 99US-0142996P.  
 XX (PION-) PIONEER HI-BRED INT INC.  
 XX Helentjaris TG;  
 XX WPI; 2001-031929/04.  
 XX P-PSDB; AAB48048.  
 XX New signal transduction nucleic acids and encoded proteins useful for  
 XX regulating phytohormone expression, including ethylene, auxins,  
 XX cytokinins and gibberellin, to provide control of plant response to  
 XX environmental stresses.  
 XX Claim 1; Page 95-96; 126pp; English.  
 XX The invention provides Zea mays signal transduction proteins and encoding  
 XX nucleotide sequences. The nucleic acids are useful for regulating  
 XX expression of phytohormones, including ethylene, auxins, cytokinins, and  
 XX gibberellin, to effect developmental changes in plants and provide  
 XX control of plant response to environmental stresses. They may also be  
 XX used as probes or amplification primers in the detection, quantitation or  
 XX isolation of gene transcripts, for detecting mutations in the gene, for  
 XX monitoring upregulation of expression or changes in enzyme activity in  
 XX screening assays of compounds, for detection of any number of allelic  
 XX variants, or for site-directed mutagenesis in eukaryotic cells. They may

CC further be used for recombinant expression of their encoded polypeptides,  
 CC as immunogens in the preparation or screening of antibodies, and in sense  
 CC or antisense suppression of genes in a host cell, tissue or plant. The  
 CC proteins may be used in assays for enzyme agonists or antagonists, as  
 CC immunogens or antigens to obtain antibodies specifically immunoreactive  
 CC with the proteins. The present sequence represents a cDNA encoding a  
 CC signal transduction protein of the invention  
 CC  
 XX SQ Sequence 1197 BP; 317 A; 306 C; 281 G; 293 T; 0 U; 0 Other;

Query Match 36.7%; Score 513; DB 4; Length 1197;  
 Best Local Similarity 67.4%; Pred. No. 9.2e-36;  
 Matches 739; Conservative 0; Mismatches 355; Indels 3; Gaps 1;

QY 87 GCGCGGTGCGGAGTTTCAGGCGCATGATGACGACGCGCGCGCGTACCTGCTCTAGAC 146  
 DB |||||  
 QY 103 GGGATGATGAGAACATCCACGCGACGCTCAGCCACGCGTGGCGCTTCATCCAGTACAC 162  
 DB |||||  
 QY 147 ATCTTCGGGAACAGTTTCGAGGTGACGAACAAGTACCGCGCGCCCATCATGCCCATTTGGC 206  
 DB |||||  
 QY 163 ATCTTCGGGAACAGTTTCGAGGTGACCTCCAGATACAAAGCCGCCCATCTCCCATCGGC 222  
 DB |||||  
 QY 207 CGCGCGCCTACCGGATCGTCTGCTCGTGTGATGAATTTTGAGACGAGGAGATGTTGGCG 266  
 DB |||||  
 QY 223 AAGGCGCCTACCGCATGCTCTGCTCGCGCTCACTCCGAGACGGCAGAGGTGGCC 282  
 DB |||||  
 QY 267 ATAAGAAGATGCGCAACCGCTTCAACACGACATGGAACGCCCAAGCGCACGCTCCGGGAG 326  
 DB |||||  
 QY 283 ATCAAGAAGATGCGCAACCGCTTCAACACGACATGGAACGCCCAAGCGCACGCTCCGGGAG 342  
 DB |||||  
 QY 327 ATCAAGCTCTCAGGACCTCGACACGACGACGACGACGACGACGACGACGACGACGACG 386  
 DB |||||  
 QY 343 ATCAAGCTGCTCGGCCACATGGACCCACGAGAATATTGTTGCAATTAAGAGATATCATACCT 402  
 DB |||||  
 QY 387 CCGCGCATCCTCAGGCGTTCAACGAGCTCTACATCCGACGAGCTCATGGACACCGAC 446  
 DB |||||  
 QY 403 CCTCCATTGAGGAGGCAATTCATGATGTATATGCTTATGCTTATGATGATGATGATGAT 462  
 DB |||||  
 QY 447 CTCATCATCATCATCTCGCTCAACCAAGAACTGTTCAGAAAGACATGCCAGTATTTCTGT 506  
 DB |||||  
 QY 463 CTGCATCAAAATTTTCGTTCAAAAGCTTTGTTCAGAGGAGCACTGTCAAGTATTTTCTT 522  
 DB |||||  
 QY 507 TACAGATCTCGCGGCGCTCAAGTACATCCACTCGCGGACGATGATCCACCGGACCTG 566  
 DB |||||  
 QY 523 TATCAAAATCTTCGTGCTTGAAGTATATACATTCAGCAAAATGCTTCACCGGACCTG 582  
 DB |||||  
 QY 567 AAGCGGAGCAACTGCTGTCGACGCAACTGCGACCTCAAGATCTCGGACTTCGGGCTG 626  
 DB |||||  
 QY 583 AAGCTAGCAATCTTCTTTGATGCAAACTGTGACCTCAAGATATGATGATTTTGGGCTT 642  
 DB |||||  
 QY 627 GCGCGCGCTGTCGAGAGCGACATGATGACGAGTACGTTGCTCACCCTGGTGTACCGC 686  
 DB |||||  
 QY 643 GCTCGCACCACTCAGAAACGATTTTATGACTGAATATGTTGTCAAGATGATATAGA 702  
 DB |||||  
 QY 687 GCGCGGAGCTGCTGCTCAACTCAACGACTACTCCGCGGCATCGAGCTGTGCTCGTC 746  
 DB |||||  
 QY 703 GCACGAGAGCTTTTATTTGAACTCTCTGAAATATATCTGTGCAATGATGTGTGCTGTG 762  
 DB |||||  
 QY 747 GGTGTCATCTTCAGGAGCTCATCAACCGCCAGCGCTCTTCCCGCGGACGACCATG 806  
 DB |||||  
 QY 763 GCTGTATATTTATGAACTGATGGACCGAAACCTTTGTTCTCGAAGATCATGTC 822  
 DB |||||  
 QY 807 CACAGATGCGCCTCATCACCGAGGTGATCGGAGCGCGGACGAGCTGGGGTTC 866  
 DB |||||  
 QY 823 CATCAGCTACGCTACTAATGAGCTCTTGGAAACCGAATAGGCTGATCTTGNATTT 882  
 DB |||||  
 QY 867 ATACGGAACGAGGACGCGAGGAAGTACATGAGGACCTCGCGGAGTACCGCGCGGACG 926  
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 QY 883 GTA---AATGAAATGCAAGAAGATATATTCGCCAACTTCCTGTCTATGCTAGACAGTCC 939  
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 QY 927 TTCGCGAGCATGTTCCGCGGGTTCAGCGCGCGCTTCGACCTCATCGAGAGATGCTC 986  
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 QY 940 TTCCTGMAAATTTCCACATGTATACACCTTTAGCAATTGACCTAGTGTGAAAGATGCTA 999  
 DB |||||

QY 987 ACCTTCAACCCGCTGCGAGAGATCAAGTTTGGAGCGCTCGATCATCTTACCTAGAG 1046  
 DB |||||  
 QY 1000 ACTTTTATCTTATGATCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 1059  
 DB |||||  
 QY 1047 AGATTGCGAGCATCGCCGATGAGCCCATCTGCTCGGAGCCCTTCTCTCGACTTCGAG 1106  
 DB |||||  
 QY 1060 TCATTTTCATGACATAAGTGTGATGAGCCAGTCTGCTCAATGCCCTTCAGCTTCGACTTCGAG 1119  
 DB |||||  
 QY 1107 CAGAAGGCTTAAACGAGGACCAATGAAGAGCTGATCTTCAACGAGGATCGAGATG 1166  
 DB |||||  
 QY 1120 CAGCATGCAATATCTGAAGACAGATGAAGGATCTGATCTACCAAGAGGCTCTTGCATTC 1179  
 DB |||||  
 QY 1167 AACCCAAACATCGGTA 1183  
 DB |||||  
 QY 1180 AACCCAGATTACCGTA 1196  
 DB |||||

RESULT 8

AAC84262  
 ID AAC84262 standard; cDNA; 1197 BP.  
 XX AC AAC84262;  
 XX AC AAC84262;  
 DT 19-MAR-2001 (first entry)  
 XX Signal transduction protein encoding cDNA.  
 DE Zea mays; maize; signal transduction protein; phytohormone; ethylene;  
 KW auxin; cytokinin; gibberellin; immunogen; ss.  
 KW Zea mays.  
 OS Zea mays.  
 FH Key  
 CDS 1..1197  
 FT /tag= a  
 FT /product= "signal transduction protein"  
 XX

WO200070059-A2.

23-NOV-2000.

28-APR-2000; 2000WO-US011687.

14-MAY-1999; 99US-0134292P.

08-JUL-1999; 99US-0142996P.

(PION-) PIONEER HI-BRED INT INC.

Helentjaris TG;

WPI; 2001-031929/04.

P-PSDB; AAB48047.

New signal transduction nucleic acids and encoded proteins useful for regulating phytohormone expression, including ethylene, auxins, cytokinins and gibberellin, to provide control of plant response to environmental stresses.

Claim 1; Page 92-93; 126pp; English.

The invention provides Zea mays signal transduction proteins and encoding nucleotide sequences. The nucleic acids are useful for regulating expression of phytohormones, including ethylene, auxins, cytokinins, and gibberellin, to effect developmental changes in plants and provide control of plant response to environmental stresses. They may also be used as probes or amplification primers in the detection, quantitation or isolation of gene transcripts, for detecting mutations in the gene, for monitoring upregulation of expression or changes in enzyme activity in screening assays of compounds, for detection of any number of allelic variants, or for site-directed mutagenesis in eukaryotic cells. They may further be used for recombinant expression of their encoded polypeptides, as immunogens in the preparation or screening of antibodies, and in sense



CC or antisense suppression of genes in a host cell, tissue or plant. The  
CC proteins may be used in assays for enzyme agonists or antagonists, as  
CC immunogens or antigens to obtain antibodies specifically immunoreactive  
CC with the proteins. The present sequence represents a cDNA encoding a  
CC signal transduction protein of the invention  
XX  
SQ Sequence 1197 BP; 306 A; 307 C; 292 G; 292 T; 0 U; 0 Other;

Query Match 36.6%; Score 511.2; DB 4; Length 1197;  
Best Local Similarity 67.2%; Pred. No. 2.2e-95;  
Matches 739; Conservative 0; Mismatches 358; Indels 3; Gaps 1;

QY 84 GGGCGCGCGTGGGAGTTTCAGCGCGAGCATGACGACGCGCGCGCTGCTCTCTAC 143  
Db 100 GCGGTGATGTTGGACAACATCCAGCGAGCGCTCAGCCAGCGGCGCGCTTCATCCAGTAC 159

QY 144 GACATCTTCGGGAACAAAGTTGAGAGGTGACGAACAAGTACAGCGCGCGCATGATGCCCAT 203  
Db 160 AACATCTTCGGCAACGTTTCGAGGTACCGCGCAAGTACAAAGCCCGCTCTCCCGCATC 219

QY 204 GCGCGCGCGCTACGCGATCGTCTGCTCGTGTGATGAATTTGAGAGCGAGGAGATGGTG 263  
Db 220 GGCAGGCGCGCTACGCGATCGTCTGCTCGCGCTCACTCCGAGCGCGGAGCGAGGTG 279

QY 264 GCGATAAAGAGATGCGCAACGCGTTTCAACAACGACATGGAAGCGCAAGCGCTCCGG 323  
Db 280 GCCATCAAGAAGATGCGCAAGCGCTTCGACAACAAGATCGATGCCAAGCGCGCTCCGC 339

QY 324 GAGATCAGTCTCTAGGCACTCTGACGACGAGGAACATCATAGGATCAGGGATGTGATC 383  
Db 340 GAGATCAAGCTGCTCGGCCACATGAGCACGAGAAATATTTGCAATAAGGGGAATCATA 399

QY 384 CCGCGCGCGATCCTCAGGCGTTCAACGAGTCTACATCGCCACGAGCTCATGGACACC 443  
Db 400 CTTCTGCGCAGAGGCTGATTCATATGATGTGTATATGATATGATATGATGATGAT 459

QY 444 GACCTCCATCATCATCTCCGCTCAACCAAGAACTGTTCAGAAAGCACTGCCAGTATTTTC 503  
Db 460 GATCTGATCAATATTTGTTCAATCAAGCTTTGTGAGAGGACACTGTCAATATTTT 519

QY 504 CTGTACAGATCTGCGGGGCTCAAGTACATCACTCGGCGAACTGATCCACCGGAC 563  
Db 520 CTTTATCAATCTCTGCTGCTTGAAGTATATACATTCAGCAATGTCTTCCACCGTAC 579

QY 564 CTGAGCGGAGCAACTGCTGCTGAAAGCGCAACTGCGACCTCAAGATCTGCGACTTCGG 623  
Db 580 TTGAAGCTAGCAATCTCTTTTGAATGCAAACTGTGACCTCAAGATATGTGATTTGGG 639

QY 624 CTGCGCGCGCTGCTGAGAGCGCATGATGACGAGTACGTGTGTACCCGGTGGTAC 683  
Db 640 CTTGCTGCGCACCTCAGAACTGATTTTATGACTGAAATATGTTGTCAAGATGGTAT 699

QY 684 CCGCGCGGAGTGTGCTCAACTCAACGACTCTCGCGCGCATTCGACGTCTGGTCC 743  
Db 700 AGAGCACGAGCTTTTGTGAACTCTCAGAAATATATCTGCTGCCATCGATGTGTGTCT 759

QY 744 GTGCGTGCATCTTCAGGAGCTCATCAACCGCGCGCTCTTCCCGCAGGAGACCA 803  
Db 760 GTGCGCTGTATATTTATGGAAGTGTGAGCGGCAAACTCTTGTCTCGAAGAGACCAT 819

QY 804 ATGCACAGATGCGCTCATCACCGAGGTGATCGGACGCGCGGACGAGCACTGGGG 863  
Db 820 GTCCATCAGCTACGTCTTCTAATGAGCTCATTTGGCAGCGCAATGAGGGTGTATTTGAT 879

QY 864 TTCATACGGAACGAGGACGCGAGAGTACATGAGGCACTCGCGCGCATACCGCGCGCG 923  
Db 880 TTTTGTATAAATGCAAGAGATATATCCGCCAACTTCTCTGTCACCTTAGACAG 936

QY 924 ACGTTGCGGAGCATGTTCCGCGGGTGCAGCCCGCGCTCGCACTCATTCGAGAGATG 983  
Db 937 TCCTTACCTGAAATTTTCCACATGTATCAACCTTTAGCAATGACCTTGGTGGAAAGATG 996

QY 984 CTCACCTTCAACCGCGTGCAGAGAAATCAAGTTGAGGAGCGCTCGATCATCTTACCTTA 1043

Db 997 CTGACTTTTGTATCTTAGACAGAGAATAAAGTTGAAGCGCACTTGCACACCCCTTACTTG 1056  
QY 1044 GAGAGATTGACGAGATCGCCGATGAGCCCATCTGCTGGAGCCCTTCTCTTCGACTTC 1103  
Db 1057 GCATCACTTCATGACATAAGTGATGAGCGAGGCTGCTCAATGCCCTTCAGCTTTGACTTC 1116  
QY 1104 GAGCAGAAGGCTCTAAACGAGGACCAAAATGAAGCAGCTGATCTTCAACGAAGCGATCGAG 1163  
Db 1117 GAGCAGCATGCTTCTGAGAACAAATGAAGGATCTTATCTACCAAGAGGCTCTTGCA 1176

QY 1164 ATGAACCCAAACATCCGTA 1183  
Db 1177 TTCAACCCCTGATTATCAGTA 1196

RESULT 9  
AAC43105  
ID AAC43105 standard; DNA; 1188 BP.  
XX AAC43105;  
XX AC AAC43105;  
XX 17-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 38047.  
XX  
XX Hybridization assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway; metabolic pathway;  
KW promoter; termination sequence; ss.  
XX  
OS Arabidopsis thaliana.  
XX  
PN EP1033405-A2.  
XX  
XX 06-SEP-2000.  
XX  
XX 25-FEB-2000; 2000EP-00301439.  
XX  
XX 25-FEB-1999; 99US-0121825P.  
PR 05-MAR-1999; 99US-0123180P.  
PR 09-MAR-1999; 99US-0123548P.  
PR 23-MAR-1999; 99US-0125788P.  
PR 25-MAR-1999; 99US-0126264P.  
PR 29-MAR-1999; 99US-0126785P.  
PR 01-APR-1999; 99US-0127462P.  
PR 06-APR-1999; 99US-0128234P.  
PR 08-APR-1999; 99US-0128714P.  
PR 16-APR-1999; 99US-0129845P.  
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PR 21-APR-1999; 99US-0130449P.  
PR 23-APR-1999; 99US-0130510P.  
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PR 28-APR-1999; 99US-0131449P.  
PR 30-APR-1999; 99US-0132048P.  
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PR 07-MAY-1999; 99US-0132863P.  
PR 11-MAY-1999; 99US-0134256P.  
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PR 25-MAY-1999; 99US-0136021P.  
PR 27-MAY-1999; 99US-0136392P.  
PR 28-MAY-1999; 99US-0136782P.



PR 01-JUN-1999; 99US-0137222P.  
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PR 18-JUN-1999; 99US-0139763P.  
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PR 01-JUL-1999; 99US-0141842P.  
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PR 08-JUL-1999; 99US-0142803P.  
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PR 16-AUG-1999; 99US-0149368P.  
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PR 23-AUG-1999; 99US-0149902P.  
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PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
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PR 06-OCT-1999; 99US-0157865P.  
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PR 08-OCT-1999; 99US-0158232P.  
PR 12-OCT-1999; 99US-0158369P.  
PR 13-OCT-1999; 99US-0159293P.  
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PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161922P.  
PR 28-OCT-1999; 99US-0161933P.  
PR 29-OCT-1999; 99US-0162142P.

Query Match		36.4%; Score 508.8; DB 3; Length 1188;
Best Local Similarity		67.2%; Pred. No. 6.7e-95;
Matches 736; Conservative 0; Mismatches 357; Indels 3; Gaps 1;		
QY	92	GGTGGCGAGTTCAGCGCGAGATGACGACGCGCGCGTACTCTCTACGACATCTT 151
DB	96	GATTGAGATATTCCCGCGACTCTTAGCCATGTGTGTAGTTTATTTCAGTATACATATT 155
QY	152	CGGGAACAAGTTCGAGGTGACGAACAAGTACCAAGCGCGCCCATCATGCCATTGGCGCG 211
DB	156	TGGAACATCTTCGAGGTACCGCTAAGTATAAGCTCCGATCATGCTATTGGCAAGG 215
QY	212	CGCTACGAGATCGTCTGCTCGTGTGATGAATTTGAGACGAGGAGATGTGGCGATAA 271
DB	216	TGCTTATGGCATCGTTTGTTCGGCTATGAATTTGAACTTAACGAGAGCGTTGCGATTAA 275
QY	272	GAAGATCGCAACCGCTTCAACACGACATGGAAGCGCAAGCGCACCTCGGAGATCAA 331
DB	276	GAATAATGCTAACGCTTTTGACAATTAAGATTGATGCTAAGAGGACTCTCCGTGAGATCAA 335
QY	332	GCTCCTCAGGACCTCGACCACGAGAACATCATAGGCATCAGGGATGTGATCCCGCGGC 391
DB	336	GCTGCTTGGTCAATGATCATGAATATATTGTCATCAGAGATATTATCCGCGACC 395
QY	392	GATCCCTCAGGCGTTCAACGAGTCTACATGCGCAAGAGCTCATGGAACAGCACTCCA 451
DB	396	ATTAAGAAACGCTTTCAACGATGTTTACATCGCGTATGAGTTAATGACACTGATCTCCA 455
QY	452	TCACATCATCGCTCCAAACCAAGAACTGTGAGAGAGCACTGCCAGTATTTCCTGTACCA 511
DB	456	TCAATCATTCGGTCAATCAAGCATATCCGAAGAACATTTGCCAGTATTTTCTTTACCA 515
QY	512	GATCCTCGCGGGGCTCAAAGTACATCCACTCGGCGAAGCTGATCCACCGGACCTGAAGCC 571
DB	516	GATCCTCGGTGATTGAATATACATTCACCTGCAATATGCTTCACAGGATTTGAAACC 575
QY	572	GAGCAACCTGCTCTGAAACGCAACTGCGGACCTCAAGATCTGCGAATTCGGGTGGCGG 631
DB	576	AAGTAATCTCTCTGAAACGCAACTGCGGACCTCAAAATCTGCGATTTTGGGTAGCTCG 635
QY	632	CGCGTCTCGGAGAGGACATGATGACGAGTACGTGCTCACCCTGCTGACCGCGCC 691
DB	636	AGTCACTTCGAGAGTATTTTCATGACTGAATATGTTGTCAGAGATGTACCGTGCACC 695
QY	692	GGAGCTGCTGCTCAACTCCACCGACTACTCGCGCCATCGAGCTCTGTGCTCGGCTG 751
DB	696	AGAGCTTCTTAAACTTCTCTGATTATATCTGAGTATCGATGTTTGTCTGTAGGCTG 755
QY	752	CATCTTCATGGAGCTCATCAACCGCAGCGCTCTTCCCGGAGGAGGACCAATGACCA 811
DB	756	TATTTTTCATGGAGTTAATGGACGTAAGCCACTCTTCCCTGGACGAGATCATGTCCATCA 815
QY	812	GATGCGCTCATCACCGAGTGTATCGGAGCGCGAGGACGAGCTGGGTTCATAG 871
DB	816	GCTTCGCTGCTCATGAGCTCATAGAACTCCATCAGAGAGAGCTGAGTTCTT--- 872
QY	872	GAACGAGGAGCGGAGGAAGTACATGAGGCACTTCGCGCAGTACCCGCGCGGACGTTCCG 931
DB	873	GAACGAAGCGCAAGGATACATATAGACAGCTTCCACCTTATCTCGCCATCCATCAC 932
QY	932	GAGCATGTTCCCGGGGTGAGCGCGCGGCTCGACCTCATCGAGAGAGTCTACCTT 991
DB	933	TGATAAGTTTCCCGACAGTGCATCTTTAGCTATAGACCTTATCGAGAAGATGTTACAT 992
QY	992	CAACCGCTGCAGAGATCACAGTTCGAGGCGCTCGATCATCTCTTACTAGAGAGATT 1051
DB	993	TGATCTTAGACGAGAGATCACAGTTTTCAGACGATTTGGGCCATTCATCTGAATCTGTT 1052
QY	1052	GCAAGCATCGCGATGAGCCCATCTGCTGAGAGCCCTTCTCTTCGACTTCGAGCAGAA 1111
DB	1053	GCAAGCATTAAGCATGAGCCAGAGTGTACAATACCTTTCAACTTTGATTTTGAAACCA 1112
QY	1112	GGCTCTTAACGAGGACCAATTAAGCAGCTGATCTTCAAGGAAGCATCGAGATGAACCC 1171

DB	1113	TGCACTCTCAGAGGAGCAGATGAAGAACTAATCTACCGCGAGCGCTTGCTTTCAATCC 1172
QY	1172	AAACATCCGGTACTAG 1187
DB	1173	AGNATATCAGCAATAG 1188
RESULT 10		
ABZ12839		
ID	ABZ12839	standard; DNA; 1188 BP.
XX	ABZ12839;	
XX	21-JAN-2003	(first entry)
DE	Arabidopsis thaliana	stress regulated gene SEQ ID NO 644.
XX	Arabidopsis thaliana;	plant; gene; stress; transgenic; de.
OS	Arabidopsis thaliana.	
PN	WO200216655-A2.	
XX	28-FEB-2002.	
XX	24-AUG-2001;	2001WO-US026685.
PR	24-AUG-2000;	2000US-0227866P.
PR	26-JAN-2001;	2001US-0264647P.
PR	22-JUN-2001;	2001US-0300111P.
XX	(SCRI )	SCRIPPS RES INST.
PA	(SYGN )	SYNGENTA PARTICIPATIONS AG.
PI	Harper JF,	Kreps J, Wang X, Zhu T;
XX	WPI;	2002-304127/34.
PT	Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.	
PS	Claim 144; SEQ ID NO 644; 577pp + Sequence Listing; English.	
CC	The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office	
XX	Sequence 1188 BP; 333 A; 273 C; 256 G; 326 T; 0 U; 0 Other;	
Query Match 36.4%; Score 508.8; DB 6; Length 1188;		
Best Local Similarity 67.2%; Pred. No. 6.7e-95;		
Matches 736; Conservative 0; Mismatches 357; Indels 3; Gaps 1;		
QY	92	GGTGGCGAGTTCAGCGCGAGATGACGACGCGCGCGTACTCTCTACGACATCTT 151
DB	96	GATTGAGATATTCCCGCGACTCTTAGCCATGTGTGTAGTTTATTTCAGTATACATATT 155
QY	152	CGGGAACAAGTTCGAGGTGACGAACAAGTACCAAGCGCGCCCATCATGCCATTGGCGCG 211
DB	156	TGGAACATCTTCGAGGTGACCGCTAAGTATAAGCTCCGATCATGCTATTGGCAAGG 215
QY	212	CGCTACGAGATCGTCTGCTCGTGTGATGAATTTGAGAGCGGAGATGTGGCGATAA 271

Db 216 TGCTTATGGCATGTTTGTTCGGCTATGATCTGAACTAACGAGCGTTCCGATTAA 275  
Qy 272 GAAGATGCGCAACGCGTTTCAACCAACGACATGAGCGCAAGCGCACCGCTCCGGGAGATCAA 331  
Db 276 GAAATATGCTTAACGCTTTTGAACAATAAGATTGATCTAAGAGGAGCTCTCCGTGAGATCAA 335  
Qy 332 GCTCCTCAGGCACTCGACACGACAGACATCATAGGATCAGGATGATCCCGCGCC 391  
Db 336 GCTGCTTCGTGCATCGATCATGAAATATATTTGCAATCAGAGATTAATTCGCCGACCC 395  
Qy 392 GATCCCTCAGGCGCTTCAACGACGCTCTACATCGCCAGCGAGCTCATGACACCGACCTCCA 451  
Db 396 ATTAAGNAACGCTTTCAACGATCTTACATCGCGTATGATTAATGACACACTGATCTCCA 455  
Qy 452 TCACATCATCGCTTCAACCAACGAACTGTGAGAAGAGCACTGCGCAGTATTTCTCTGTACCA 511  
Db 456 TCAATCATTCGGTCAATCAAGCAATATCCGAAGAACATTTGCCAGTATTTCTTTTACCA 515  
Qy 512 GATCTCGGGGCTCAAGTACATCATCTCCGCGACGCTGATCCACGCGACCTGAAGCC 571  
Db 516 GATCTCCGCGGATGAATATACATCTCACTGCAAAATGTCCTTACAGGAGATTTGAAACC 575  
Qy 572 GAGCAACCTCTGCTGTAACGCCAACTCGGACCTCAAGATCTGCGACTTCGGGCTGGCGG 631  
Db 576 AAGTATCTCTCTGNAACGCAACTGCGACCTAANAATCTGCGATTTGGGCTAGCTCG 635  
Qy 632 GCGCTCGTGGAGAGCGACATGATGACGGAGTACGTGGTCAACCGGTGGTACCGCGCCG 691  
Db 636 AGTCACCTTCGTGAGAGTATTTCACTGATGATGTTGTCACGAGATGGTACCGTGCACC 695  
Qy 692 GGAGCTGCTCTCACTCCACCGACTACTCCGCGCCATCGAGTCTGGTCCGTCCGCTG 751  
Db 696 AGAGCTTCTCTTAACTCTTCTGATTAATCTGAGCTATCGATGTTTGGTCTGTAGGCTG 755  
Qy 752 CATCTTCATGAGCTCATCAACCGCAGCGCGCTCTTCCCGCGAGGACACATGACACCA 811  
Db 756 TATTTTCATGAGATTAATGACCGTAAAGCACTCTTCCCTGGACGAGATCATGTCCATCA 815  
Qy 812 GATCGCGCTCATCAACGAGTGTATCGGAGCGCCGCGAGCGACGAGCTGGGGTTCAACG 871  
Db 816 GCTTGGCTTCTCATGAGCTCATAGGACTCATAGAACTCCATCATGAAGAAGAGCTCGAGTCTT--- 872  
Qy 872 GAACGAGGAGCGAGGAGTACATGAGGACACTGCGCGAGTACCGCGCGGAGCTTCGC 931  
Db 873 GAACGAAACGCAAGCGATACATAGACAGCTTCCACCTTATCTCGCCCAATCCATCAC 932  
Qy 932 GAGCATGTTCCCGGGTGACGCGCGCGCTCGACCTCATCGAGAGGATGCTCAACCTT 991  
Db 933 TGATAAGTCCGACAGTGCATCTTTAGCTATAGACCTTATCGAAGATGTTAATTT 992  
Qy 992 CAACCCGCTGCAGAGATCAAGTTGAGGAGCGCTCGATCATCTTTACCTAGAGAGATT 1051  
Db 993 TGATCTTAGAGGAGATCAAGTTTATAGAGCATTTGGCCCATCCATACCTGAATCGTT 1052  
Qy 1052 GCAGCATCGCGATGAGCCATCTCCCTGGAGCCCTTCTCTTGCATTCGATTCGAGAGAA 1111  
Db 1053 GCAGCATAGCGATGAGCGAGAGTGTACAATACCTTTCAACTTTTGAATTTTGAACCA 1112  
Qy 1112 GGCTCTAAACGAGCAACCAATGAAGCAGCTGATCTTCAACGAGCGATCGAGATGAACCC 1171  
Db 1113 TGCACCTCTAGAGAGAGATGAAGAACTAATCTACCGGAGCGCTTCTTCTTCAATCC 1172  
Qy 1172 AAACATCCGGTACTAG 1187  
Db 1173 AGAATATCAGCAATAG 1188

RESULT 11

ADX47615

ID ADX47615 standard; cDNA; 1637 BP.

XX

AC ADX47615;

XX

DT 21-APR-2005 (first entry)  
XX Plant full length insert polynucleotide seqid 22355.  
XX plant protectant; plant growth regulant; gene therapy; plant;  
KW recombinant DNA construct; physical array; plant breeding marker;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
KW growth rate; cell cycle pathway; disease resistance;  
KW galactomannan production; lignin production; plant growth regulator;  
KW yield; plant growth; plant development; seed oil; protein yield;  
KW protein content; gene; ss.  
XX Unidentified.  
OS US2004034888-A1.  
XX PN 19-FEB-2004.  
XX 28-APR-2003; 2003US-00425114.  
XX PF 06-MAY-1999; 99US-00304517.  
XX PR 05-NOV-2001; 2001US-00985678.  
XX PA (LIU/) LIU J.  
XX PA (ZHOU/) ZHOU Y.  
XX PA (KOVA/) KOVALIC D K.  
XX PA (SCRE/) SCREEN S E.  
XX PA (TABA/) TABASKA J E.  
XX PA (CAOV/) CAO Y.  
XX PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
XX WPI; 2004-180133/17.  
XX New recombinant DNA construct, useful for improving plant tolerance to  
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
PT pests, for conferring increased resistance to plant disease, or for  
PT improving yield.  
XX Claim 1; SEQ ID NO 22355; 15pp; English.  
XX The invention describes a recombinant DNA construct comprising a  
CC polynucleotide consisting of a sequence encoding an amino acid sequence  
CC available in electronic form from the US patent office at  
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide  
CC of the invention are also useful in physical arrays of molecules and as  
CC plant breeding markers. The recombinant DNA construct is useful for  
CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
CC plant cells by modification of the cell cycle pathway, for conferring  
CC increased resistance to plant disease, for producing galactomannan,  
CC lignin or plant growth regulators, for increasing the rate of homologous  
CC recombination in plants, for improving yield by modification of  
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
CC or by providing improved plant growth and development under at least one  
CC stress condition or for modifying seed oil or protein yield and/or  
CC content. This sequence represents a plant full length insert  
CC polynucleotide that can be used in the recombinant DNA construct of the  
CC invention.  
XX Sequence 1637 BP; 420 A; 434 C; 381 G; 402 T; 0 U; 0 Other;

Query Match 35.3%; Score 492.2; DB 13; Length 1637;

.Best Local Similarity 65.1%; Pred. No. 1.9e-91;

Matches 725; Conservative 0; Mismatches 388; Indels 0; Gaps 0;

Qy 81 GACGGGCGCGCGTGGCGAGTTTCAGCGCGACGATGACGACGCGCGCGGTACCTGCTC 140

Db 221 GCGGAGGAGGAGGAGCGGAGATCAAGGGTATGGCGACGACGCGGGGCGCGCTACGTGCTG 280

Qy 141 TAGGACATCTTCGGGAACAAGTTCGAGGTGACGAACAAGTACCAGCGCCCATCATGCC 200

Db 281 TACAAGTGTACGGGAACCTCTTCGAGGTCTCTCCAAAGTACGCCCGGCCCATCCGCCCC 340  
Qy 201 ATTGGCGCGCGCCCTTACCGGATCGTCTGCTCGTATGAATTTTGAGACGAGGGAGATG 260  
Db 341 ATCGCGCGCGCGCTACGGCAATGCTCGCGCGCTGTCAACTCACAGACAGGGAGGAA 400  
Qy 261 GTGGCGATAAAGATCGCAACGGGTTCAACAGCAATGACGCGCAAGCGCAGCTC 320  
Db 401 GTTGGCATCAAGAGGTGTGCAATGCGTTTCGACACCAATGACGCGCAAGCGCAGCTG 460  
Qy 321 CGGAGATCAAGTCTCTCAGGCACTCGACCGAGAAATATAGGCAATGACGCGGATG 380  
Db 461 AGGAGATCAAGTCTCGGCAATGACGCAATGACGCAATGACGCAATGACGCAATG 520  
Qy 381 ATCCCGCGCGCGATCCCTCAGGCGTTCAACGAGCTTACATCGCCACGAGCTCATGGAC 440  
Db 521 ATACGCGCGCGCACTAGAGAGAACTTTAATGACGTGTACATTGTACTGAGTTAATGGAT 580  
Qy 441 ACCGACTCCATCACATCATCCGCTCCACCAAGAACTGTGACAGGCACTGCCAGTAT 500  
Db 581 ACAGATCTCCATCAGATCATACGCTCAAAATCAGCCATTTGACTGATCATCTGCCAGTAC 640  
Qy 501 TTCTGTACAGATCTCTCGGCGGCTCAAGTACATCCATCGCGCAACGTGATCCACCGC 560  
Db 641 TTCTGTATCAGTTGCTAGAGGGCTAATATATGTGCACTCAGCAATATATTTGACCGC 700  
Qy 561 GACCTGAAGCGGAGCAACTGTGCTGAACGCACTCGGCACTCAAGATCTGCGACTTC 620  
Db 701 GATCTAAGCGGAGCAATTTGTTCTTAATGCAATTTGTGACCTCAAGATCGCAGACTTT 760  
Qy 621 GCGCTGGCGCGCGCTGTGAGAGGAGGACATGACGAGGATGATGCTGCTACCCGGTGG 580  
Db 761 GCGCTTTCAGAGGACCACTCAGAGACAGATCTCATGACAGAGTATGTGCTCACTCGTGG 820  
Qy 681 TACGCGCGCGGAGCTGTCTCAACTCCACGACTACTCGCGCGCATCGAGCTCTG 740  
Db 821 TACAGGCGCAGAGCTGTGTTGAATCTTTCAGTACACTGCTGCTGCTGCTGCTGCTG 880  
Qy 741 TCGCTGCGGTGATCTTCATGAGCTCATCAACCGCGAGCGCTCTTCCCGCGCAGGAC 800  
Db 881 TCAGTTGGATGATATTTAGTGAATCGTTACTCGCCAACTGTTTCTGCGACGGAT 940  
Qy 801 CATGACACAGATGCGCTCATCAGGAGTGTATCGGAGCGCGGAGGAGGAGGAGCTG 860  
Db 941 TACATCCAGCTTAAATTTGATCAGCGAGCTCATAGGCTCACCAGATGATCAAGCCTG 1000  
Qy 861 GCGTTTCATACGGAACGAGGACGAGGAGTACATGAGCACTGCGCGAGTACCGCGC 920  
Db 1001 GGATTTCTTGAAGTATATGCAAAAGATATGAAACAACTACACAGTTTCCAAG 1060  
Qy 921 CGGAGCTTCGCGAGCATGTTCCGCGGGTGCAGCGCGCGCTCGACCTCATCGAGAGG 980  
Db 1061 CAGGACTTCGCGCTGCTTCCGTAACATGCTCTGCTGCTGCTGCTGCTGCTGCTG 1120  
Qy 981 ATGCTACCTTCAACCGCTGAGAGAAATGAGTTGAGGAGCGCTGATCATCTTAC 1040  
Db 1121 ATGCTTGTGTTGATCCAGCAGACGAGTTACAGTTGATGAGGCTCTGCACTACCCATAC 1180  
Qy 1041 CTAGAGAGATTCAGACATTCGCGGATGAGCCATCTGCTGAGCGCTTCTCTTCGAC 1100  
Db 1181 TTGCTTCACTTATGATCATTAATGAAAGAACCTTACCTGCGCTGCACTTTCAGCTTGTAT 1240  
Qy 1101 TTGAGCAGAGGCTCTTAAACGAGGACCAATGAAGCAGCTGATCTTCAACGAGGAGTAC 1160  
Db 1241 TTTGAGCAACCATCTTTTACAGAGCGCATATAAAGAACTTATCTGGAGGAATCTTTA 1300  
Qy 1161 GAGATGACCAACATCCGGTACTAGATTGAA 1193  
Db 1301 GCATTTAACCCGATCTCTCCCTACTAATTTCAA 1333

RESULT 12  
ADX53699

ID ADX53699 standard; cDNA; 1520 BP.  
XX AC ADX53699;  
XX DT 21-APR-2005 (first entry)  
XX DE Plant full length insert polynucleotide seqid 28439.  
XX KW plant protectant; plant growth regulant; gene therapy; plant;  
KW recombinant DNA construct; physical array; plant breeding marker;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
KW growth rate; cell cycle pathway; disease resistance;  
KW galactomannan production; lignin production; plant growth regulator;  
KW yield; plant growth; plant development; seed oil; protein yield;  
KW protein content; gene; ss.  
XX OS Unidentified.  
XX FN US2004034888-A1.  
XX PD 19-FEB-2004.  
XX PF 28-APR-2003; 2003US-00425114.  
XX PR 06-MAY-1999; 99US-00304517.  
XX PR 05-NOV-2001; 2001US-00985678.  
XX PA (LIU/) LIU J.  
XX PA (ZHOU/) ZHOU Y.  
XX PA (KOVA/) KOVALIC D K.  
XX PA (SCRE/) SCREEN S E.  
XX PA (TABA/) TABASKA J E.  
XX PA (CAO/) CAO Y.  
XX PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
XX WIPI; 2004-180133/17.  
XX New recombinant DNA construct, useful for improving plant tolerance to  
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
PT pests, for conferring increased resistance to plant disease, or for  
PT improving yield.  
XX PS Claim 1; SEQ ID NO 28439; 15pp; English.  
XX CC The invention describes a recombinant DNA construct comprising a  
CC polynucleotide consisting of a sequence encoding an amino acid sequence  
CC available in electronic form from the US patent office at  
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide  
CC of the invention are also useful in physical arrays of molecules and as  
CC plant breeding markers. The recombinant DNA construct is useful for  
CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
CC plant cells by modification of the cell cycle pathway, for conferring  
CC increased resistance to plant disease, for producing galactomannan,  
CC lignin or plant growth regulators, for increasing the rate of homologous  
CC recombination in plants, for improving yield by modification of  
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
CC or by providing improved plant growth and development under at least one  
CC stress condition or for modifying seed oil or protein yield and/or  
CC content. This sequence represents a plant full length insert  
CC polynucleotide that can be used in the recombinant DNA construct of the  
CC invention.  
XX SQ Sequence 1520 BP; 393 A; 351 C; 367 G; 409 T; 0 U; 0 Other;  
Query Match 34.8%; Score 485.8; DB 13; Length 1520;  
Best Local Similarity 64.8%; Pred. No. 3.8e-90;  
Matches 721; Conservative 0; Mismatches 392; Indels 0; Gaps 0;  
QY 81 GACGGGCGCGGTGCGGAGTTTCAGGCGGAGGATGACGAGGCGCGGTACCTGCTC 140

Db 38 GGGGGCGGCGTGGAGCCGAGATCAAGGGTATGGCGACGCAAGGGGGCGCTACGTGCTG 97  
Qy 141 TAGACATCTTCGGGAAACAAGTTTCGAGGTGACGAACAAGTACAGCGCCGCCATCATGCCC 200  
Db 98 TACAACGTGTAGCGGAACCTCTTCGAGGTCTCTCCAAAGTACGCGCCCAACCCATCGCGCCC 157  
Qy 201 ATTGGCGGCGGCGCTACGGGATCGTCTGCTCGGTGATGAATCTTGAGAGCGAGGAGTG 260  
Db 158 ATCGGTGCGGCGGCGCTACGGCATCTGTCTGGCGGCTGTCAACTCGCAGTCAGGGAGGAG 217  
Qy 261 GTGGCCATAGAAGATCGCCACGCGTTCAACAACGACATGACGCCCAAGCGCAGCTC 320  
Db 218 GTTGCAATCAGAGGTTGGCATGTGTTGCAACAACCATGACGCCAAGCGGAGCTC 277  
Qy 321 CGGAGATCAAGCTCTCAGGCACTCGACCAAGAAACATCATAGGCATCAGGGATG 380  
Db 278 AGGGAATCAAGCTGTGGCCACATGACCAATGCAACATCTTCCCTTAAAGGATGA 337  
Qy 381 ATCCCGCGCGCATCCCTCAGGGGTTCAAGCGGTCTACATCGCAGCGAGCTCATGGAC 440  
Db 338 ATTCGGCCCCCACTAGAGAGAACTTTAATGAGCTGTACATTTACTGAGTTAATGGAT 397  
Qy 441 ACCGACTCATCATCATCTCCGCTCCAAACCAAGAACTGTCAAGAGCACTGCCAGTAT 500  
Db 398 ACAGATCTCCATCAGATCGTACGCTCAATCAGCCATTGACTGATGATCATTTGCCAGTAC 457  
Qy 501 TTCCTGTAACAGATCTCGGGGGCTCAAGTACATCCATCTGGCGAACGTGATTCACCGC 560  
Db 458 TTCTTGTATCAGTTGTTACGAGGGCTAAATATGTGCACTCAGCAAAATATATTGCCACCG 517  
Qy 561 GACCTGAGCGGAGCAACCTGTCTGTAAGCGCACTCGGACCTCAAGATCTGGACTTC 620  
Db 518 GATCTGAAGCGGAGCAATTTGTTCTTAAATGCAAAATTTGACCTCAAGATTGCAGACTT 577  
Qy 621 GGGCTGGCGGCGCTGCTCGGAGAGCGACATCATGACGAGTACGTGGTCAACCCGGTG 680  
Db 578 GGGCTTGCAGAGACCACTTCAGAGACAGATCTCATGACAGATATGTGTCACTCTGTGG 637  
Qy 681 TACCGCGCGCGGAGCTGTCTCAACTCAGGACTACTCGCGCCCATTCGACGCTG 740  
Db 638 TACCGGCGCACAGCTGCTGTTGAATGTTTACAGTATCTGCTGCCATTGATGCTG 697  
Qy 741 TCGTGGCTGATCTTCATGAGCTCATCAACCGCGCGGCTCTTCCCGGCGAGGAC 800  
Db 698 TCAGTTGGATGCATCTAGGTGAATCGTTACTCTGTCGTAACCCCTGTTTCTGGACGGAT 757  
Qy 801 CACATCACCAGATCGCCTCATCACGAGGTGATCGGGACGCGGACGAGCAGAGCTG 860  
Db 758 TACATCAGCATTAATAATTGATCACTGAGCTCATAGGCTCTCCAGATGATGAGCCTG 817  
Qy 861 GGGTTTCATCGGAACGAGGACGCGAGAGTACATGAGGCACCTGCGCGCAGTACCGCGC 920  
Db 818 GGATTTCTTGAAGTATATGCAAAAGATACATGAACAACATCCACAGTTTCCAAGA 877  
Qy 921 CGGAGCTTCGCGAGCATGTTCCGCGGGTGCAGCGCGCGCTCGACCTCATCGAGAG 980  
Db 878 CAGGACTTCGCGCTGCGGTTTTCCGCAACATGCTCTCTGGCGCAGTCGATTTGTTGAAAG 937  
Qy 981 ATGCTACCTTCAACCGCTGCAGAGAAATCACAAGTTGAGGAGGCGCTCGATCATCTTAC 1040  
Db 938 ATGCTGTGTTGATTCAGCAGACGGAATTACAGTTGATGAGGCTCTGCATCATCCATAC 997  
Qy 1041 CTAGAGAGATTGCACGATCGCGGATGAGCCCATCTGCTCGGAGCGCTTCTCTCTCGAC 1100  
Db 998 TTGGCTTCACTTCATGAGATCAATGATGAACTTACCTGCGCTGCACCTTTCAGCTTGTAT 1057  
Qy 1101 TTGAGCAGAGGCTCTAAACGAGGACCAATGAGCAGCTGATCTTCAAGAGGAGATC 1160  
Db 1058 TTTGAGCAACCATCTTTTACAGAGCGCATATAAAGAACTCATCTGGAGGGAATCTTTA 1117  
Qy 1161 GAGATGAACCAACATCCGGTACTAGATTGAA 1193  
Db 1118 GCATTTAACCCAGAGCCTCCCTACTATATCA 1150

RESULT 13  
AAC43674

ID AAC43674 standard; DNA; 1546 BP.

XX AAC43674;

XX 18-OCT-2000 (first entry)

XX Zea mays DNA fragment SEQ ID NO: 40086.

XX Hybridisation assay; genetic mapping; gene expression control;  
XX protein identification; signal transduction pathway; metabolic; pathway;  
XX promoter; termination sequence; corn; ss.

XX Zea mays subsp. mays.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

XX 05-MAR-1999; 99US-0123180P.

XX 09-MAR-1999; 99US-0123548P.

XX 23-MAR-1999; 99US-0125788P.

XX 25-MAR-1999; 99US-0126264P.

XX 29-MAR-1999; 99US-0126785P.

XX 01-APR-1999; 99US-0127462P.

XX 06-APR-1999; 99US-0128234P.

XX 08-APR-1999; 99US-0128714P.

XX 16-APR-1999; 99US-0129845P.

XX 19-APR-1999; 99US-0130077P.

XX 21-APR-1999; 99US-0130449P.

XX 23-APR-1999; 99US-0130510P.

XX 23-APR-1999; 99US-0130891P.

XX 28-APR-1999; 99US-0131449P.

XX 30-APR-1999; 99US-0132048P.

XX 30-APR-1999; 99US-0132407P.

XX 04-MAY-1999; 99US-0132484P.

XX 05-MAY-1999; 99US-0132485P.

XX 06-MAY-1999; 99US-0132486P.

XX 07-MAY-1999; 99US-0132487P.

XX 11-MAY-1999; 99US-0132863P.

XX 14-MAY-1999; 99US-0134218P.

XX 14-MAY-1999; 99US-0134219P.

XX 14-MAY-1999; 99US-0134221P.

XX 14-MAY-1999; 99US-0134370P.

XX 18-MAY-1999; 99US-0134768P.

XX 19-MAY-1999; 99US-0134941P.

XX 20-MAY-1999; 99US-0135124P.

XX 21-MAY-1999; 99US-0135353P.

XX 24-MAY-1999; 99US-0135629P.

XX 25-MAY-1999; 99US-0136021P.

XX 27-MAY-1999; 99US-0136392P.

XX 28-MAY-1999; 99US-0136782P.

XX 01-JUN-1999; 99US-0137222P.

XX 03-JUN-1999; 99US-0137528P.

XX 04-JUN-1999; 99US-0137502P.

XX 07-JUN-1999; 99US-0137724P.

XX 08-JUN-1999; 99US-0138094P.

XX 10-JUN-1999; 99US-0138540P.

XX 10-JUN-1999; 99US-0138847P.

XX 14-JUN-1999; 99US-0139119P.

XX 16-JUN-1999; 99US-0139452P.

XX 16-JUN-1999; 99US-0139453P.

XX 17-JUN-1999; 99US-0139492P.

XX 18-JUN-1999; 99US-0139454P.

XX 18-JUN-1999; 99US-0139455P.

XX 18-JUN-1999; 99US-0139456P.

PR	18-JUN-1999,	99US-0139457B,
PR	18-JUN-1999,	99US-0139458P,
PR	18-JUN-1999,	99US-0139459P,
PR	18-JUN-1999,	99US-0139460P,
PR	18-JUN-1999,	99US-0139461P,
PR	18-JUN-1999,	99US-0139462P,
PR	18-JUN-1999,	99US-0139463P,
PR	18-JUN-1999,	99US-0139750S,
PR	18-JUN-1999,	99US-0139763P,
PR	21-JUN-1999,	99US-0139817P,
PR	22-JUN-1999,	99US-0139899P,
PR	23-JUN-1999,	99US-0140353P,
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PR	30-JUN-1999,	99US-0141087P,
PR	01-JUL-1999,	99US-0141842P,
PR	02-JUL-1999,	99US-0142154P,
PR	02-JUL-1999,	99US-0142055P,
PR	06-JUL-1999,	99US-0142803P,
PR	08-JUL-1999,	99US-0142930P,
PR	09-JUL-1999,	99US-0143202P,
PR	12-JUL-1999,	99US-0143297P,
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PR	14-JUL-1999,	99US-0143624P,
PR	15-JUL-1999,	99US-0144005P,
PR	16-JUL-1999,	99US-0144085P,
PR	18-JUL-1999,	99US-0144086P,
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PR	20-JUL-1999,	99US-0144632P,
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PR	22-JUL-1999,	99US-0145087P,
PR	22-JUL-1999,	99US-0145089P,
PR	23-JUL-1999,	99US-0145192P,
PR	23-JUL-1999,	99US-0145152P,
PR	23-JUL-1999,	99US-0145151P,
PR	23-JUL-1999,	99US-0145218P,
PR	23-JUL-1999,	99US-0145528P,
PR	23-JUL-1999,	99US-0145224P,
PR	25-AUG-1999,	99US-0145376P,
PR	02-AUG-1999,	99US-0146388P,
PR	02-AUG-1999,	99US-0146389P,
PR	03-AUG-1999,	99US-0147038P,
PR	04-AUG-1999,	99US-0147204P,
PR	04-AUG-1999,	99US-0147302P,
PR	05-AUG-1999,	99US-0147192P,
PR	05-AUG-1999,	99US-0147260P,
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PR	28-OCT-1999	99US-0161933P
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PR	29-OCT-1999	99US-0162142P

Query Match 34.7%; Score 484.2; DB 3; Length 1546;  
Best Local Similarity 64.7%; Pred. No. 8.2e-90;  
Matches 720; Conservative 0; Mismatches 393; Indels 0;

Qy	81	GACGGGGCGCGGTGGCGGAGTTTCAGGCCGACGATGACGACGCGCGCGCGGTACTGCTC	140
Db	156	GGCGGCGCGGTGGAGCGCAGATCAAGGGTATGGCGACGACGCGGCGCGCTACGTGCTG	215
Qy	141	TACGACATCTTCGGGAACAGTTTCGAGGTGACGAACAGTACCACGCCGCCCATCATGCC	200
Db	216	TACAACGTGTACGGAAACCTCTTCGAGGTCTCTTCCAAGTACGCCCCACCCATCCGCCCC	275
Qy	201	ATTGGCGCGCGCGCTACGGGATCGTCTGCTCCGTGATGAATTTTGAGACGAGGAGATG	260

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Db 276 ATCGTCCGCGCCTACGSCATTGCTCGCGGCTGTCACTCGCAGTCAGGGAGGAG 335
Qy 261 GTGCGGATTAAGAAGATGCGCAACGGGTTCACAAACGACATGACGCGCAAGCCACGCTC 320
Db 336 GTTGGCATCAAGAAGGTGGAATGCGTTTCGACACCAACATCGACGCGCAAGCGGCTC 395
Qy 321 CGGAGATCAAGCTCTCAGCGACCTCGACCAACGAGAACATAGGACATCAGGATG 380
Db 396 AGGGAATCAAGCTGCTCGGCCACATGACCATGAGAACATCTTGGCTTTAAAGGATGA 455
Qy 381 ATCCCGCGCGGATCCCTCAGGGGTTTCAACGAGTCTTACATCGCCACGAGCTCATGGAC 440
Db 456 ATTGCGGCCCACTAGAGAGAACTTTAATGACGTGTACATTGTACTGAGTTAATGGAT 515
Qy 441 ACCGACTCATCATCATCATCCGCTCAACCAAGAACTGTGACAAAGCACTGCCAGTAT 500
Db 516 ACAGATCTCCATCAGATCGTACGCTCAATCAGCCATTTGACTGATCATATTGCCAGTAC 575
Qy 501 TTCCTGTACAGATCTCGCGGGGCTCAAGTACATCCACTCGGCGAACGTGATCCACCGC 560
Db 576 TTCCTGTATCAGTTGTACGAGGCTTAAATATGTGCACCTCAGCAATATATTGCAACCGC 635
Qy 561 GACTGAAGCGGAGCAACCTGCTGCTGAACGCGCAACTGCGACCTCAAGATCTCGACTTC 620
Db 636 GATCTGAAGCGGAGCAATTTGTTCTTAAATGCAATTTGTGACCTCAAGATTGCAACTTT 695
Qy 621 GGGCTGGCGCGCGCTCGTTCGAGAGCGACATGATGACGAGTACGTTGGTCAACCGGTGG 680
Db 696 GGGCTTGCAGGACCACTTCAGAGACAGATCTCATGACAGATGATGTGTCACCTCGTTGG 755
Qy 681 TAGCGCGCGGAGCTGCTCACTCAACGACCTACTCCGCGGCTCAAGTCTGAGTCTGG 740
Db 756 TAGCGGACACAGAGCTGCTGTTGAACTGTTCAAGTATCTGTCGCCATTGATGTCGTG 815
Qy 741 TCGTCTCGGCTGCTCTTCACTGAGCTCATCAACCGCGCGGCTCTTCCCGCGAGGAC 800
Db 816 TCAATTGGATGCTACTAGTGAATGTTACTGCTCAACCCCTGTTCTTGACGAGGT 875
Qy 801 CACATGACACAGATGCGCTCATCACCGAGGTGATCGGACGCGCGAGCGACGAGCTG 860
Db 876 TACATCCAGCAATTAATAATTTGATCCTGAGCTCATAGGCTCTCCAGATGATGCAAGCCTG 935
Qy 861 GGGTTCTACGGAACGAGGACGCGAGGAGTACATGAGGACCTGCGCGAGTACCGCGC 920
Db 936 GGAATTTCTCGAAGTGAATATGCAAAAGATACATGAACCACTTACCACAGTTTCCAAGA 995
Qy 921 CGGACGTTTCGCGAGCATGTTCCGCGGGTGCAGCCCGCGCTCGACCTCATCGAGAGG 980
Db 996 CAGACTTCCGCGCTGCGTTTCCGCAACATGTTCTCTGCGCGAGTCTGATTTGTGAAAGG 1055
Qy 981 ATGCTCACTTCAACCCGCTGCGAGAGATCACAGTTGAGGAGGCGCTCGATCATCTTAC 1040
Db 1056 ATGCTTGTGTTGATCCAAAGCAGACGAGTATACAGTTGATGAGGCTCTGCAATCATCCATAC 1115
Qy 1041 CTAGAGAGATGACGACATCGCGGATGAGCCCATCTGCTGAGGCGCTTCTCTTCCGAC 1100
Db 1116 TTGGCTTCACTTATGAGATCAATGATGAACCTTACCTGCGCGACCTTTTCAAGTTGAT 1175
Qy 1101 TTGAGCAGAAAGGCTCTTAAACGAGGACCAATGAAGCAGCTGATCTTCAACGAGCGATC 1160
Db 1176 TTTGAGCAACATCTTTACAGAGCGCATATAAAGAACTCATCTGGAGGATCTTTA 1235
Qy 1161 GAGATGAACCAACATCCGCTACTAGATTGAA 1193
Db 1236 GCATTTAAACCAAGACCTCCCTACTAATATCAA 1268
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RESULT 14  
AAV27563  
ID AAV27563 standard; cDNA; 1544 BP.  
XX  
AC  
AAV27563;

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DT 22-SEP-1998 (first entry)
XX Salicylic acid induced MAP kinase encoding cDNA.
DE Salicylic acid induced protein; SIP; mitogen-activated protein; MAP;
XX Salicylic acid induced protein; SIP; mitogen-activated protein; MAP;
KW tobacco; disease resistance; microbial pathogen; MAP kinase; de.
XX Nicotiana sp.
XX Key Location/Qualifiers
CDS 129..1310
FT /tag= a
FT /product= "salicylic acid induced MAP kinase"
XX
XX WO9818939-A1.
XX 07-MAY-1998.
XX 24-OCT-1997; 97WO-US019219.
XX 25-OCT-1996; 96US-002980SP.
XX 21-APR-1997; 97US-00837593.
XX (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
XX Klessig DF, Zhang S;
XX WPI; 1998-272230/24.
XX P-PSDB; AAW61252.
XX Salicylic acid induced MAP kinase - obtained from tobacco, used to
XX produce plants having increased disease resistance, against e.g.
XX microbial pathogens.
XX Claim 11; Page 21-22; 97pp; English.
XX This cDNA encodes a salicylic acid induced protein (SIP) kinase. This SIP
XX kinase is an unique member of the mitogen-activated protein (MAP) kinase
XX family. The salicylic acid induced MAP kinase of the invention comprises
XX kinase subdomains I to XI of serine/threonine kinases. The protein is
XX activated by an agent that induces a disease response in plants
XX by way of a signal transduction pathway that is at least partially
XX dependent on salicylic acid. Host plant cells transformed with a vector
XX containing a recombinant DNA molecule encoding the salicylic acid induced
XX MAP kinase is used to produce the protein recombinantly. The products can
XX be used to produce plants with increased disease resistance. The products
XX may also be used as a research tool to identify other proteins involved
XX in the hypersensitive response and systemic acquired response in plants
XX
XX Sequence 1544 BP; 449 A; 294 C; 335 G; 466 T; 0 U; 0 Other;
Qy Query Match 34.7%; Score 484; DB 2; Length 1544;
Best Local Similarity 65.6%; Pred. No. 9e-90;
Matches 722; Conservative 0; Mismatches 375; Indels 3; Gaps 1;
Qy 84 GGGGCGCGGTGCGGAGTTTCAGCGCGACGATGACGCGCGCGCGGTACCTGCTCTAC 143
Db 207 GTGCGCGGTATGATTAATATTCGCGCGACGTTTCAGCGCGCGGTTCATTCATATC 266
Qy 144 GACATCTTCGGGAACAAAGTTTCGAGGTGAGCAACAGTACCAGCGCGCCATCATGCCCAT 203
Db 267 AATATATTTGGTAAATATATTTGAAGTTACTGCTAAATATTAAGCTCTCTATTTTGCCTATT 326
Qy 204 GCGCGCGCGGCTTACGGGATCGTCTGCTCGTGAATCTTTGAGACGAGGAGATGGTG 263
Db 327 GGTAAAGGTGCTTACGGCATCGTTTCTGCTTTGAACTTCGAGACAAATTGAGACGTA 386
Qy 264 GCGATAAAGAGATCGCCCAACGCGTTTCAACACGACATGACCGCCAGCCACGCTCCGG 323
Db 387 GCGATAAAGAAAATCGCAATGCTTTTGTATAACAAGATTGATGCCAAGAGGACTTTGAGA 446
Qy 324 GAGATCAAGCTCTCAGGACACCTTCGACCGAGAACATCATAGGCATCAGGATGTCATC 383
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Db 447 GAGATCAAGCTTCTTCGGCATATGGATCATGAACAATTTGTTCCGATCAGAGATATAATT 506  
 Qy 384 CGCGCGCGATCCCTCAGCGGTTCAACGAGCTTACATCGCCACGAGCTCATGGACACC 443  
 Db 507 CCACCAACACAGAGAGGCTTTAATGATGTTTATTTATTTGCGTATGAGCTTATGGATCT 566  
 Qy 444 GACCTCCATCACAATCATCGCTCCCAACCAAGAACTGTCAAGAGAGACCTGCCAGTATTTTC 503  
 Db 567 GATCTCCATCAAAATTTCTGCTCTAATCAGGGTTTATCTGAGGAGCACTGTCAATTTTC 626  
 Qy 504 CTGTACACAGATCTCGCGGGGCTCAAGTACATCCACTCGCGGAACTGTGATCCACCGGAC 563  
 Db 627 TTGTATCAGATCTCGCGGGTTGAATAATACATATTTCTGCGAATGTTCTGCACAGGAC 686  
 Qy 564 CTGAAGCCGAGCAACTGCTGCTGTAAGCGCAACTGCGGACCTCAAGATCTGCGACTTTCCGG 623  
 Db 687 TTGAAGCTTGAATCTCTGTTGAATGCAACTGTGATTTAAGATATGTTATTTGGG 746  
 Qy 624 CTGGCGCGGCGCTGCTCGGAGAGCGACATGATGACGAGTACGTGTCTACCGGTTGTATC 683  
 Db 747 CTAGCTCGTGTCACTTCTGAACCTGACTTTATGACGGAATATGTTGTGACAAAGATGTTAT 806  
 Qy 684 CGCGCGCGGAGTGTCTCAACTCCACGACTACTCCGCGGCACTGACGCTGTGGTCC 743  
 Db 807 CGTCCACCTGAGCTGTTGTTAAATCTGTGACTATATCTGCAGCAATTCGACGTATGGTCA 866  
 Qy 744 GTGGGCTGCATCTTCATGAGCTCATCAACCGCGCGCTCTTCCCGCGGAGGACAC 803  
 Db 867 GTGGGTTGATTTTCAATGATGATGACAGAAACCCCTATTTCTGTGATGATCATC 926  
 Qy 804 ATGACACAGATGCGCTCATACCGAGGTGATCGGAGCGCGGACCGGACGACGAGCTGGGG 863  
 Db 927 GTACACCGCTGCTTATATGAGGTTGATTTGTTGTTACTCTTTCAGAGGCTGAAATGGAG 986  
 Qy 864 TTCAATAGGAAACGAGACCGGAGGAAGTACATGAGGCACTGCGGAGTACCGCGCGCG 923  
 Db 987 TTTTFTA---AATGAGAAATGCAAAACGATACATCCGCCAACTTCTCTTTACCGTGACAA 1043  
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 Qy 1104 GAGCAGAGGCTCTAAACGAGGACCAAAATGAACGAGCTGATCTTCAACGAAGCGATCGAG 1163  
 Db 1224 GAACAGATGCTCTTACGGAGGAAACAGATGAGAGGCTGATTTACAGGAGTGCCTTGCA 1283  
 Qy 1164 ATGAACCCAAACATCCGGTA 1183  
 Db 1284 TTTAATCTGAATACCAGCA 1303

RESULT 15

AAC84253  
 ID AAC84253 standard; cDNA; 1119 BP.

AC AAC84253;

XX 19-MAR-2001 (first entry)

DT Signal transduction protein encoding cDNA.

DE Zea mays; maize; signal transduction protein; phytohormone; ethylene;  
 KW auxin; cytokinin; gibberellin; immunogen; ss.

XX Zea mays.

XX Key Location/Qualifiers  
 FH 1..1119  
 FT /\*tag= a  
 FT /product= "signal transduction protein"  
 XX WO200070059-A2.  
 XX 23-NOV-2000.  
 XX 28-APR-2000; 2000WO-US011687.  
 XX 14-MAY-1999; 99US-0134292P.  
 PR 08-JUL-1999; 99US-0142996P.  
 XX (PION-) PIONEER HI-BRED INT INC.  
 XX Helentjaris TG;  
 XX WPI; 2001-031929/04.  
 DR P-PSDB; AAB48044.  
 XX New signal transduction nucleic acids and encoded proteins useful for  
 PT regulating phytohormone expression, including ethylene, auxins,  
 PT cytokinins and gibberellin, to provide control of plant response to  
 PT environmental stresses.  
 XX Claim 1; Page 83-85; 126pp; English.  
 XX The invention provides Zea mays signal transduction proteins and encoding  
 CC nucleotide sequences. The nucleic acids are useful for regulating  
 CC expression of phytohormones, including ethylene, auxins, cytokinins, and  
 CC gibberellin, to effect developmental changes in plants and provide  
 CC control of plant response to environmental stresses. They may also be  
 CC used as probes or amplification primers in the detection, quantitation or  
 CC isolation of gene transcripts, for detecting mutations in the gene, for  
 CC monitoring upregulation of expression or changes in enzyme activity in  
 CC screening assays of compounds, for detection of any number of allelic  
 CC variants, or for site-directed mutagenesis in eukaryotic cells. They may  
 CC further be used for recombinant expression of their encoded polypeptides,  
 CC as immunogens in the preparation or screening of antibodies, and in sense  
 CC or antisense suppression of genes in a host cell, tissue or plant. The  
 CC proteins may be used in assays for enzyme agonists or antagonists, as  
 CC immunogens or antigens to obtain antibodies specifically immunoreactive  
 CC with the proteins. The present sequence represents a cDNA encoding a  
 CC signal transduction protein of the invention  
 XX Sequence 1119 BP; 290 A; 282 C; 268 G; 279 T; 0 U; 0 Other;  
 SQ  
 Query Match 34.6%; Score 483.6; DB 4; Length 1119;  
 Best Local Similarity 64.8%; Pred. No. 1e-89;  
 Matches 717; Conservative 0; Mismatches 389; Indels 0; Gaps 0;  
 Qy 81 GACGGGCGCGGTCGGGAGTTTACGGCGAGATGACGACGCGCGCGGCTACCTGCTC 140  
 Db 13 GCGCGCGCGGTGGAGCGCAGATCAAGGGTATGGCGACGACGCGGGCGCTACGTCGTG 72  
 Qy 141 TACGACATCTTCGGGACAAAGTTTCAGGTGAGAAACAGTACAGCCCGCCCATCATGCC 200  
 Db 73 TACAACGTTACGGAACCTCTTCGAGGTCTCTCAAGTACGCCCAACCATCCGCCCC 132  
 Qy 201 ATTGGCCGCGCGCTACGGGATCGTCTGCTCCGTGATGAACCTTTTGAGACGAGGGAGATG 260  
 Db 133 ATCGGTGCGGCGCTACGGCATTTGTCTGCGGCTGTCACTCGCAGTCAGGGAGGAG 192  
 Qy 261 GTGGCGATTAAGAAGATGCCAACCGGTTCAACAGCAGATGAGACGCGGCGCGCTC 320  
 Db 193 GTTGGCATCAGAAGGTTGGCAATGCGTTTCGAAACCAACATGACGCGCAAGCGCTC 252  
 Qy 321 CGGGAGATCAAGCTCTCAGGCACCTCGACACGAGAACATCATAGGCATCAGGAGATG 380  
 Db 253 AGGGAATCAAGCTCTGCTGCCACCATGGACCATGAAACATCTTGCCTTAAGGATGA 312

Qy 381 ATCCGCGCGGATCCCTCAGGCGTTCAACGAGCTTACATCGCCCGAGCTCATGGAC 440  
Db |||||  
Qy 313 ATTGCGCCCCCACTAGAGAACTTAAATGACGTGTACATTGTTAGTGAATTAATGGAT 372  
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Qy 441 ACCGACCTCCATCACATCATCCGCTCAACCAAGAACTGTCAAGAGAGCACTGCCAGTAT 500  
Db |||||  
Qy 373 ACAGATCTCATCAGATCGTACGCTCAATCAGCCATTGACTGATGATCATTTGCCAGTAC 432  
Db |||||  
Qy 501 TTCTGTACAGATCTCTGGGGGCTCAAGTACATCCACTTCGGCGAAAGTGATCCACCGC 560  
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Qy 433 TTCTGTATCAGTTGTACGAGGGCTAAATAATATGTGCACTCAGCAATAATTGCCACCGC 492  
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Qy 561 GACCTGAAGCGGAGCACTGTCTGAAAGCCAACTGCGACCTCAAGATCTGGACTTC 620  
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Qy 493 GATCTGAAGCGGAGCAATTGTTCTTAAATGCAAAATGTGACCTCAAGATTGCAGACTTT 552  
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Qy 621 GGGCTGGCGGCGCTGCTCGGAGAGCGCATGATGACGGAGTACGTGGTCAACCGGTGG 680  
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Qy 553 GGGCTTGCAGGACCACTTCAGAGACAGATCTCATGACAGATATGTGGTCACTCGTTGG 612  
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Qy 681 TACCGCGCGCGGAGCTGTCTCAACTCCACCGACTACTCCGCGCCATCGACGTCTGG 740  
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Qy 613 TACCGGSCACAGAGCTGTGTTGAACGTGTTCAAGTATACTGCTGCCATTGATGCTGG 672  
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Qy 741 TCCGTGGGCTGCATCTTCATGGAGCTCATCAACGCGAGCGCTCTTCCCGGAGGGAC 800  
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Qy 673 TCAGTTGGATGTCATCTAGGTGAATCGTTACTCGTCAACCCCTGTTTCTGGACGGAT 732  
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Qy 801 CACATGCACAGATGCGCCTCATCCGAGGTGATCGGACGCCGAGCGAGAGCTG 860  
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Qy 1041 CTAGAGAGATTGCACGACATCGCGGATGAGCCCATCTGCTGGAGCCCTTCTCCTTCGAC 1100  
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Qy 973 TTGGCTTCACTTCATGAGATCAATGATGAACCTACCTGCCCTGCACCTTTCAGCTTTGAT 1032  
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Qy 1101 TTCGAGCAGAAGGCTCTAAACGAGGACCAATGAAGCAGCTGATCTTCAACGAAGGATC 1160  
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Qy 1033 TTTGAGCAACCATCCTTTACAGAAGCGCATATAAAGAACTCATCTGGAGGAATCTTTA 1092  
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Qy 1161 GAGATGAACCCAAACATCCGGTACTA 1186  
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Qy 1093 GCATTTAACCCAGAGCTCCCTACTA 1118  
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OM nucleic - nucleic search, using sw model

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Searched: 1303057 seqs, 888780828 residues

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	484	34.7	1544	2	US-08-837-593-1
2	483.2	34.6	1725	3	US-09-623-034-1
3	444	31.8	1718	3	US-09-828-313-21
4	337.2	24.2	1866	3	US-08-909-742-1
5	337.2	24.2	1866	3	US-09-412-289-1
6	337.2	24.2	1896	3	US-09-417-197-38
7	334	23.9	1875	3	US-09-417-197-56
8	319.8	22.9	953	3	US-09-828-313-8
9	318	22.8	1747	2	US-08-176-620A-1
10	318	22.8	1747	2	US-08-463-862-1
11	318	22.8	1747	2	US-08-461-985-1
12	318	22.8	1747	2	US-08-458-887-1
13	318	22.8	1747	3	US-08-932-787B-1
14	318	22.8	1747	3	US-08-932-012C-1
15	318	22.8	1747	3	US-08-888-818C-1
16	312.2	22.4	2826	3	US-09-949-016-3926
17	312.2	22.4	2828	3	US-09-016-434-1458
18	312.2	22.4	2980	3	US-09-266-225D-11
19	292.6	21.0	1502	2	US-08-651-940-1
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21	292.6	21.0	1502	3	US-09-724-768-1
22	291	20.8	1134	3	US-09-949-016-3997
23	289.6	20.7	1310	3	US-09-047-288-1
24	289.6	20.7	1310	3	US-08-802-191-1

25 288.6 20.7 1457 3 US-09-949-016-3988  
26 279.2 20.0 1851 2 US-08-674-612-1  
27 279.2 20.0 1851 2 US-08-700-575-45  
28 279.2 20.0 1851 2 US-08-920-296-1  
29 279.2 20.0 1851 3 US-09-124-163-1  
30 278.8 20.0 1095 3 US-09-809-464-2  
31 278.8 20.0 1259 3 US-09-809-464-3  
32 278.8 20.0 1839 3 US-09-949-016-5420  
33 276.8 19.8 1834 3 US-09-016-434-419  
34 274.8 19.7 1260 2 US-08-029-404-1  
35 274.8 19.7 1260 3 US-08-459-953A-1  
36 274.8 19.7 1260 2 US-09-393-212-1  
37 273.6 19.6 1838 2 US-08-746-788-1  
38 273.6 19.6 1838 3 US-09-189-602-1  
39 265 19.0 2180 3 US-09-286-904-23  
40 265 19.0 2180 3 US-09-640-101-23  
41 265 19.0 2180 3 US-09-016-434-1140  
42 258 18.5 1611 3 US-08-909-742-2  
43 258 18.5 1611 3 US-09-412-289-2  
44 258 18.5 1701 3 US-09-949-016-4048  
45 258 18.5 2791 3 US-09-016-434-1263

ALIGNMENTS

RESULT 1  
US-08-837-593-1  
; Sequence 1, Application US/08837593  
; Patent No. 5977442  
; GENERAL INFORMATION:  
; APPLICANT: Klessig, Daniel F.  
; APPLICANT: Zhang Zhuqun  
; TITLE OF INVENTION: "No. 5977442 Salicylic Acid Induced  
; TITLE OF INVENTION: Map Kinase and its Use for Enhanced Disease Resistance in Pla  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman,  
; ADDRESSEE: P.C.  
; STREET: 1601 Market Street, Suite 720  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: United States of America  
; ZIP: 19103-2307  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/837,593  
; FILING DATE: April 21, 1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/029,805  
; FILING DATE: October 25, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Reed, Janet E.  
; REGISTRATION NUMBER: 36,252  
; REFERENCE/DOCKET NUMBER: Rutgers 97-0016  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 563-4100  
; TELEFAX: (215) 563-4044  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1544 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: unknown  
; MOLECULE TYPE: cdna  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO

FRAGMENT TYPE:  
ORIGINAL SOURCE: tobacco  
US-08-837-593-1

Query Match 34.7%; Score 484; DB 2; Length 1544;  
Best Local Similarity 65.6%; Pred. No. 5.4e-97;  
Matches 722; Conservative 0; Mismatches 375; Indels 3; Gaps 1;

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QY 84 GGGCGCGCGGTGGCGGAGTTTCAGGCGGACGATGACGACGCGGCGGCGGTACCTGCTCTAC 143
DB 207 GTGGCGGTATGATTAATATTCGGCGAGCTTGAGCCAGGTGGCGAGGTTCAATCAATAC 266

QY 144 GACATCTTCGGGAACAAGTTTCGAGGTGACGAACAAGTACCAGCGCCCATCATGCCATT 203
DB 267 AATATATTTGGTAATATATTTGAAGTTACTGCTAATATAAGCTCTATTTTGCCTATT 326

QY 204 GGGCGGCGGCGCTTACGGGATCGTCTGCTCGGTGATGAATTTGAGACGAGGAGATGGTG 263
DB 327 GGTAAAGGTGCTTACGGCATCGTTTCTGCTTGAACCTCGGAGCAATTTGAGAACGTA 386

QY 264 GCGATAAAGAAGATCGCAACGCTTCAACAACGACATGAGCGCAAGCGCACTCGCTCGG 323
DB 387 GCGATAAAGAAATCGAAATGCTTTTGATAACAGATTGATGCCAAGAGGACTTTGAGA 446

QY 324 GAGATCAAGCTCTCAGGCACTCGAACGAAACATCATAGGCACTCAGGGATGTGATC 383
DB 447 GAGATCAAGCTCTCAGGCACTCGAACGAAACATTTGTCGATCAGAGATATAATT 506

QY 384 CGGCGGCGGATCCTCAGGGTTCAACGAGCTTACATCGCCACGAGCTCATGAGACAC 443
DB 507 CCACCAACACAGAGAGGCGCTTAAATGATGTTTATATTCGCTATGAGCTTATGGATCT 566

QY 444 GACCTCATACATCATCGCTCCCAACCAAGRACTGTCAGAGAGCACTGCCAGTATTTTC 503
DB 567 GATCTCATCAATTAATTTGCTCTAATCAGGGTTTATCTGAGAGCACTGTCAATTTTC 626

QY 504 CTGTACAGATCTCGGGGGCTCAAGTATCATCTCAGCGCAACGTGATCCACCGCGAC 563
DB 627 TTGTATACAGATCTCCGAGGGTTGAAATACATACATCTTCGCGAATTTCTGACAGGAG 686

QY 564 CTGAACCGAGCAACTGCTGCTGAACGCGCACTGCGCACTCAAGATCTGCGACTTCGGG 623
DB 687 TTGAAGCCTAGCAATCTCCTGTTGAATGCCAATGTGATTTAAAGATATATGATTTGG 746

QY 624 CTGGCGCGGCGCTGTCGAGAGCGACATGATGACGAGTACGTGTGCTACCGGCTGTAC 683
DB 747 CTAGCTCTGTGCTACTTCTGAACTGATTTAGCGGAATATGTTGTGACAGAGATGGTAT 806

QY 684 CGCGCGCGGAGCTGCTCTCACTCACCGACTACTCGCGCGCAATCGACGCTGCTGCTCC 743
DB 807 CGTCCACCTGAGCTGTTGTTAAATCTGCTGACTACTGACGCAATTCAGCTATGCTCA 866

QY 744 GTGGCTGTGATCTTCAATGAGCTCATCAACCGCGACCGCTCTTCCCGCGGAGGACAC 803
DB 867 GTGGGTGCAATTTTTCATGAAATTTGATGCAAGAAACCCCTATTTCTGCTGAGATCAC 926

QY 804 ATGCACCAATGCGCTCATACCGAGGTGATCGGGAACCGCAACGACGAGCTGGGG 863
DB 927 GTACACAGCTGCTCTTATTTGAGAGTTGATTTGGTACTCTTTTACAGAGCTGAAATGG 986

QY 864 TTCTATACGGAACGAGGACGCGGAAGATACATGAGGCACTTGCAGAGTACCGCGCGCG 923
DB 987 TTTTFTA--AAAGAGAAATGCAAAACGATACATCCGCAACTCTCTTTACCGTGCACAA 1043

QY 924 AGTTTCGAGGATGTTTCGGGGGTGACGCGCGCGCTGTGACCTCATTCGAGAGGATG 983
DB 1044 TCATTCACCTGAAAGTTTTCACATGTACACCCCACTGCAATTTGATCTTGTTCGAGAAATG 1103

QY 984 CTCACCTTCAACCGCTGCAGAGAAATCACAGTTTGAAGGCGCTGCATCATCTTACCTTA 1043
DB 1104 CTGACATTTGATCTCTAGAGGAGAAATCAAGTTTGAAGGTTGCACTTGCACATCTTACCTG 1163

QY 1044 GAGAGATTGCAACGACATCGCCGATGAGCCCATCTGCTCGAGGCGCTTCTCTTCGAGTTC 1103
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DB 1164 AACTCGCTCCACGATATTAGTAGACGAGCCCATTTGCGATGACTCCCTTTAGCTTCGACTTT 1223
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DB 1224 GAACAGCATGCCCTTACGAGGAAACAGATGAAGGAGCTGATTTACAGGGAGTCGCTTGA 1283
QY 1164 ATGAACCCAAACATCCGGTA 1183
DB 1284 TTTAATCTCTGAATACCAGCA 1303

RESULT 2
US-09-623-034-1
; Sequence 1, Application US/09623034
; Patent No. 6765128
; GENERAL INFORMATION:
; APPLICANT: Klesbig, Daniel F.
; APPLICANT: Zhang, Shuhun
; TITLE OF INVENTION: METHODS OF USING A PATHOGEN-ACTIVATABLE
; TITLE OF INVENTION: MAP KINASE TO ENHANCE DISEASE RESISTANCE IN PLANTS
; FILE REFERENCE: RUT98-0073
; CURRENT APPLICATION NUMBER: US/09/623,034
; CURRENT FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US99/03882
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: 60/075,685
; PRIOR FILING DATE: 1998-02-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1725
; TYPE: DNA
; ORGANISM: Nicotiana tabacum
US-09-623-034-1

Query Match 34.6%; Score 483.2; DB 3; Length 1725;
Best Local Similarity 65.3%; Pred. No. 8.4e-97;
Matches 710; Conservative 0; Mismatches 378; Indels 0; Gaps 0;

QY 84 GGGCGCGCGGTGGCGGAGTTTCAGGCGGAGATGAGCGCGGCGGCGGTACCTGCTCTAC 143
DB 141 GAGGCTCAATTCCTCGATTTTCTTCGGTTTAACTCAGCGCGCAATATGTACAGTTT 200

QY 144 GACATCTTCGGGAACAAGTTTCGAGGTGACGAACAAGTACCAGCGCCCATCATGCCATT 203
DB 201 GATATTTTGGTAATTTCTTTGAGATCACTACCAAGTATCGTCTCTTATTTAGCTATT 260

QY 204 GGGCGCGGCGCTTACGGGATCGTCTGCTCGGTGATGAATTTTGAGACGAGGAGATGGTG 263
DB 261 GGTGCTGCTGCTTATGGAATTTGCTGCTCGGTGTTGAATACGAGCTGAATGAGATGGTT 320

QY 264 GGGATAAAGAGATCGCCAAACGCTTCAACAACGACATGAGCGCCCAAGCGGACGCTCCGG 323
DB 321 GCGATTAAAGAAATCGCAATCGCTTTGATATTTTACATGGGATGCTTAAGAGGACTCTCCGT 380

QY 324 GAGATCAAGCTCTCAGGCACTCGACCGACCATGAGCAACATCATAGGCACTCAGGGATGTGATC 383
DB 381 GAGATTAAGCTCTCTCGCCATTTAGACCATGAAATGTAATTTGGTTTAAAGACCTGATT 440

QY 384 CGCGCGCGGATCCCTCAGGCGTTCAAACGAGCTCTACATCGCCACGCGAGCTCATGGACACC 443
DB 441 CCTCCACCTTACGAAGGAGGTTTCTGATGTTTACATTTGCTACTGTAACTCATGGATACT 500

QY 444 GACCTCATCATCATCATCGCTCCAAACGAACTGTGAGAGAGCACTGCCAGTATTTTC 503
DB 501 GATCTTCAACCAATTAATTTAGATTCACCAAGGTTTTATCAGAGGATCACTGTCAAGTATTC 560

QY 504 CTGTACCAAGATCTCGCGGGGCTCAAGTACATCCACTCGGCGAAGCTGATCCACCGCGAC 563
DB 561 ATGATACAGCTCTCTCGGTGGCGCTAATAATACATACATATTCGCGAATGTTCTTCAAGAT 620

QY 564 CTGAAGCGGAGCAACCTCTGCTGCTGCGAAGCCCAACGCGCACTCGCAAGATCTGCGGG 623
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Db 621 CTAAACCGAGCAACCTTTGGTAATGCAANTGTGATCTTAAGATATGTGCTTGGT 680  
 Qy 624 CTGGCGCGCGCTGTCGGAGAGCGACATGATGACGGAGTACGTGGTCAACCGGTGGTAC 683  
 Db 681 CTTGCTAGGCCAAACATAGAGACGAGATATGACGGAATATGTTGTAACAGATGGTAC 740  
 Qy 684 CGCGCGCGAGCTGCTCAACTCAACCGACTACTCCGCGCATCGAGCTCTGGTCC 743  
 Db 741 AGGCGCACAGAGCTTTTGTGAACTCTTCAGATTAACATCTGCTGTATAGATGTTGGTCT 800  
 Qy 744 GTGGCTGCATCTTCATGAGCTCATCAACCGCGAGCGCTCTTCCCGCGCAGGACCA 803  
 Db 801 GTGGTTGCATCTTCATGGAACCTTATGAATAGAAAACCTTTGTTGGTGAAGAATCAT 860  
 Qy 804 ATGCACAGATGGCCCTCATCACCGAGTGTATCGGACGCGGACGACGAGCTGGGG 863  
 Db 861 GTACATCAATACGCTTGTAAACGAGCTTCTGGCACCCCAACAGAAAGCTGATCTGGC 920  
 Qy 864 TTCAATCGGAACGAGGACGCGAGGAAGTACATGAGGCACTTGGCGGAGTACCGCGCGG 923  
 Db 921 TTCTCTCAAAATGAAGATGCAAGAGATACATCAGGCAACTCCCAACAACATCTCTCGCCAG 980  
 Qy 924 AGTTTCGAGGCAATGTTCCCGGGTGCAGCCCGCGCTCGACCTCATCGAGAGGATG 983  
 Db 981 CAGTTAGCAGAAGTTTTCCTCATGTGAACCCATTTGGCTATGTATCTTGTGGAATAAATG 1040  
 Qy 984 CTCACCTTCAACCGCTGCGAGAGATCACAGTTGTGAGGAGGCTCGATCATCTTACCTA 1043  
 Db 1041 TTGACATTCGATCTACTAGAGAAATACAGTTGAGGAGGATTTAGATCATCTTACCTT 1100  
 Qy 1044 GAGAGATTGACGACATCGCGGATGACCCATCTGCTCGAGGCTTCTCTCTGACTTC 1103  
 Db 1101 GCAAGCTCCACGATGCGAGTGCAGAACCGATCTGCCCTGTTCATTTCTCTTGAATTT 1160  
 Qy 1104 GAGCAGAGGCTCTAAACGAGGACCAATGAGCAGCTGTCTTCAACGAGGATCGAG 1163  
 Db 1161 GAGCAACAGGAATAGGAGAGGCAATTAAGGACATGATATATATCAGGAAGCTTTGTCA 1220  
 Qy 1164 ATGAACCC 1171  
 Db 1221 CTGAATCC 1228

RESULT 3

US-09-828-313-21  
 ; Sequence 21, Application US/09828313  
 ; Patent No. 6867351  
 ; GENERAL INFORMATION:  
 ; APPLICANT: COSTA e SILVA, OSWALDO DA  
 ; APPLICANT: BOHNET, HANS J.  
 ; APPLICANT: THIELEN, NOCHA VAN  
 ; APPLICANT: CHEN, ROUYING  
 ; APPLICANT: SARRIA-MILLAN, RODRIGO  
 ; TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED PROTEINS AND METHODS OF  
 ; USE IN PLANTS  
 ; FILE REFERENCE: 16313-0032  
 ; CURRENT APPLICATION NUMBER: US/09/828,313  
 ; CURRENT FILING DATE: 2001-04-06  
 ; PRIOR APPLICATION NUMBER: 60/196,001  
 ; PRIOR FILING DATE: 2000-04-07  
 ; NUMBER OF SEQ ID NOS: 128  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 21  
 ; LENGTH: 1718  
 ; TYPE: DNA  
 ; ORGANISM: Physcomitrella patens  
 US-09-828-313-21

Query Match 31.8%; Score 444; DB 3; Length 1718;  
 Best Local Similarity 63.9%; Pred. No. 3.5e-88;  
 Matches 672; Conservative 0; Mismatches 380; Indels 0; Gaps 0;

Qy 111 ACGATGACGACGCGCGGTACCTGCTCTAGACATCTTCGGGAACAAGTTCGAGGTG 170  
 Db 424 ACTCCGACCTACGAGGTCAATTACGTGAATATGTTGTGGCGGAACGTATTTTCGAATC 483  
 Qy 171 ACGAAACAAGTACACAGCCGCCCATCATGCCCATTTGGCGCGGCGCTTACGCGATCGTTCG 230  
 Db 484 ACGCGAGGTACAAAGCCACCCTTTCGTCGATTTGGCGCGGAGCTTATGGAATCGTCTGT 543  
 Qy 231 TCGGTATGAACCTTTGAGACGAGGAGATGGTGGCGATTAAGAAGATCGCAACGCGTTC 290  
 Db 544 TCACTCTTTGATACCTTTACCGGTGAGGAGGTGGCGGTCAAAAAGAGTTGAAAACGCGTTC 603  
 Qy 291 AACAAACGATGACGACCCCAAGCGCAGCTCCGCGAGATCAAGCTCTCAGCAGCTCCGAC 350  
 Db 604 GACAAACAGATCGATCGAAGCGCAACACTGCTGGAATTAACCTCTCCGCGATATGGAT 663  
 Qy 351 CACGAGAACATCATAGGCATCAGGATGTGATCCCGCGCGCGATCCCTCAGGGGTTCAC 410  
 Db 664 CATGAACAAGTCTGCTGCAATACAGACATCAATTCGTCGCCCACTAGGGAGAATTTCAAC 723  
 Qy 411 GAGGTCTAATGCCACGAGGCTCATGGAACCGACCTCTCATCATCATCATCATCATCATCAT 470  
 Db 724 GAGGTCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 783  
 Qy 471 CAAGACTGTCAGAAAGCACTGCCAGATTTTCTGTACAGATCTTCCGCGGCGCTCAAG 530  
 Db 784 CAAGCTCTCAGAAAGCACTGTCAGATTTTCTGTATCAAAATCTTCCGCGGCTTGAAG 843  
 Qy 531 TACATCCACTCGCGCAACGATGATCCACCGGACCTTGAAGCCGAGCAACCTGCTGCTGAAC 590  
 Db 844 TACATCCATTCGCGGAACGCTTTCGACCGGACTTGAAGCCCAACCACTTCTGCTCAAT 903  
 Qy 591 GCCAATGCGACTCAAGATCTCGACTTCGCGCTTGGCGCGCGCGCTGCTCGGAGAGCGAC 650  
 Db 904 GCCAATGCGATTTGAAATCGCAGATTTTGGCTTGGCAGCACTCTCTCTGAAAACGAT 963  
 Qy 651 ATGATGAGGAGTACGTGGTCAACCGGTGATCGCGCGCGGCGGAGCTGCTCAACTCC 710  
 Db 964 TTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1023  
 Qy 711 ACCGACTACTCCGCGCATCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 770  
 Db 1024 TCAGCATACACTGAGCTATTTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1083  
 Qy 771 AACCGCAGCGCTTCTCCCGGAGGACCAATGACAGATGCGCTCATCACCGAG 830  
 Db 1084 AACCGATCTGCTGCTTCTCCCGGAGGACTATGTCATCAGCTCCGCTTAATTAACAGAA 1143  
 Qy 831 GTGATCGGAGCGCGAGCAGAGCTGGGTTTATAGGACGAGGAGCGAGGAG 890  
 Db 1144 CTCATCGGAACCTCTGAAGATAGGGATCTTGGGTTTGAAGACGCAATGCTAGGCGG 1203  
 Qy 891 TACATGAGCAGCTCCCGCAGTACCCGCGCGGAGCTTCGCGAGCATGTTCCCGCGGTG 950  
 Db 1204 TATATCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1263  
 Qy 951 CAGCCCGCGCTGCACTCATCGAGAGATGCTCACTTCAACCGCTGCAAGAGATC 1010  
 Db 1264 AATCGTTCTGCTCTTGTATCTTGTGAAGAGATGCTGCTTGTGATCAGCGAAGAAATC 1323  
 Qy 1011 ACAGTTGAGAGGCGCTGATCATCTTACTAGAGAGATGACAGCATCGCCGATGAG 1070  
 Db 1324 ACAGTGAAGCTGCTTGGCGCACCTTATTTAGCTTCACTTCAATCATCAACAGATGAG 1383  
 Qy 1071 CCCATCTGCTGGAGCCCTTCTCTCTCGACTTTCGAGCAGAGGCTCTAAACGAGGACCA 1130  
 Db 1384 CTTGCTCGGTATCTCTCTCGAGTTTGAATTCGAGGAGGCGCCCTATCTATCTCGAGGAGCAT 1443  
 Qy 1131 ATGAAGCAGCTGATCTTCAACGAGGATCGA 1162  
 Db 1444 ATCAAGGATCTCAATTCGAGGAGGCTCTGGA 1475

## RESULT 4

US-08-909-742-1  
; Sequence 1, Application US/08909742  
; Patent No. 6007991  
; GENERAL INFORMATION:  
; APPLICANT: Vimala S. Sivaraman  
; APPLICANT: Hsien-Yu Wang  
; APPLICANT: Craig C. Malbon  
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR MITOGEN-  
; TITLE OF INVENTION: ACTIVATED PROTEIN KINASES AS THERAPY FOR  
; TITLE OF INVENTION: BREAST CANCER  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hoffmann & Baron, LLP  
; STREET: 350 Jericho Turnpike  
; CITY: Jericho  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 11753  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for windows  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/909,742  
; FILING DATE: August 12, 1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/831,994  
; FILING DATE: April 1, 1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/827,520  
; FILING DATE: March 28, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Adams, Lindsey S.  
; REGISTRATION NUMBER: 36,425  
; REFERENCE/DOCKET NUMBER: 178-225 CIP II  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 822-3550  
; TELEFAX: (516) 822-3582  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1866 nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHEetical: NO  
; ANTI-SENSE: NO  
US-08-909-742-1

Query Match 24.2%; Score 337.2; DB 3; Length 1866;

Best Local Similarity 61.3%; Pred. No. 1.1e-64; Matches 603; Conservative 0; Mismatches 363; Indels 18; Gaps 3;

QY 182 CCAGCGCCCATCATGCCCCATTGGCGCGGCTACGGGATCGTCTGCTCCGTCATGAA 241  
Db 195 CTACACGCGATTGCACTACATCGCGGCGGCTACGGGATCGTCTGCTCCGTCATG 254  
QY 242 CTTTGGAGCAGGAGATGTTGGCGATTAAGAAGATCGCCAGCGGTTCAACACGACAT 301  
Db 255 CCACGTCGCGAAGATCGGCTGGCCATCAAGAAGAT---CAGCCCTTCGAACATCAGAC 311  
QY 302 GGACGCGCAAGCGACGCTCGGGGAGATCAAGCTCTCAGSCACCTCGACCGAGAACAT 361  
Db 312 CTAAGTCGCGCGCAGCGCTCGGGGAGATCAAGATCTCTGCTCGGCTTCGGCATGAGATGT 371  
QY 362 CATAGGCATCAGGAGATGTGATCCCGCGCGGATCCCTCAGGGCGGTTCAACGACGTCATCAT 421  
Db 372 CATCGGCATCCGAGACATCTCGGGGCGTCCACCTCGGAAGCCATGAGAGATGCTTACAT 431  
QY 422 CGCCAGGAGCTCATGAGACCGACCTCCATCATCATCATCTCCGCTCCACCAAGAACTGTC 481

Db 432 TGTGAGGACCTGATGGAGACTGACCT---GTACAAGTTGCTGAAAAGCCAGCAGCTGAG 488  
QY 482 AGAAGAGCACTGCGCAGTATTTCTGTACAGATCTCGGGGGGCTCAAGTACATCCACTC 541  
Db 489 CAATGACCATATCTGCTACTTCTCTACAGATCTCTGGGGGCTCAAGTACATCCACTC 548  
QY 542 GCGAAACGTGATCCACCGGACCTGAAGCCGAGCAACCTGTCTGTGAACGCCAATGCGA 601  
Db 549 CGCCAAACGTGCTCCACCGAGATCTAAAGCCCTCCAACCTGTCTCAGCAACACCACTCGCA 608  
QY 602 CCTCAAGATCTCGACTTCGGGCTGGCGGG-----CGTCTCGGAGAGCA 649  
Db 609 CCTTAAGATTTGTGATTTTGGGCTGGCGGGATTCGCGATCTGAGCATGACACACCGG 668  
QY 650 CATGATGACGAGTACGTGGTCAACCGGTGGTACCGCGCGCGGAGCTGCTCTCAACTC 709  
Db 669 CTTCTGACGGAGTATGTGGTACCGGCTGGTACCGGGCCCGAGAGATCATGCTGACTC 728  
QY 710 CACCGACTACTCCGCGCCATCGAGCTCTGGTCCGTGGCTGCTCATTTCTATGAGCTCAT 769  
Db 729 CAAGGGCTATACCAAGTCCATCGACATCTGGTCTGTGGGCTGCAATTTCTGGCTGAGATGCT 788  
QY 770 CAACCGCCAGCGCTCTTCCCGGCGAGGACCAATGACACGAGATGCGGCTCATCACCA 829  
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QY 830 GGTGATCGGGACCGCGAGCGAGCTGGGGTTCATACGAAACGAGAGCGCGAGAA 889  
Db 849 CATCTCTGGCTCCCATCCAGGAGACTGATTTGATCATCAACATGAAGCCCGAAA 908  
QY 890 GTACATGAGGACCTCGCGCAGTACCGCGCGGCGAGTTCGCGAGCATGTTTCCCGGGGT 949  
Db 909 CTACCTACAGTCTCTGCGCTCCCAAGCAAGGTGGCTTTGGGCAAGCTTTTCCCAAGTC 968  
QY 950 GCAGCGCGCGGCTCGACCTCATCGAGAGATGCTCACTTCAACCGCTCGAGAGAT 1009  
Db 969 AGACTCCAAAGCCCTTGACCTGTCGAGCGGATGTTAACTTTAAACCCCAATAAAGCGAT 1028  
QY 1010 CACAGTTCAGGAGCGGCTCGATCATCTTACCTAGAGAGATTCACGACATCGCGATGA 1069  
Db 1029 CACAGTGGAGAGCGCTGGCTCACCCCTCTCTGGAGGAGTACTATGACCCGACGATGA 1088  
QY 1070 GCCCATCTGCTGGAGCCCTTCTCTCTCGACTTCGAGCAGAGAGGCTCTAAACGAGACCA 1129  
Db 1089 GCCAGTGGCGAGGAGCCCTTCACTTCCCATGAGCTGGATGACCTACCTAAGAGCG 1148  
QY 1130 AATGAAGCAGCTGATCTTCAACGA 1153  
Db 1149 GCTGAAGGAGCTCATCTTCCAGGA 1172

## RESULT 5

US-09-412-289-1

; Sequence 1, Application US/09412289  
; Patent No. 6271210  
; GENERAL INFORMATION:  
; APPLICANT: Sivaraman, Vimala S.  
; APPLICANT: Wang, Hsien-Yu  
; APPLICANT: Malbon, Craig C.  
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR MITOGEN-ACTIVATED  
; TITLE OF INVENTION: PROTEIN KINASES AS THERAPY FOR CANCER  
; FILE REFERENCE: Seq. 1-4 (178-225 CIP II/CON)  
; CURRENT APPLICATION NUMBER: US/09/412,289  
; CURRENT FILING DATE: 1999-10-05  
; EARLIER APPLICATION NUMBER: 08/909,742  
; EARLIER FILING DATE: 1997-08-12  
; EARLIER APPLICATION NUMBER: 08/831,994  
; EARLIER FILING DATE: 1997-04-01  
; EARLIER APPLICATION NUMBER: 08/827,520  
; EARLIER FILING DATE: 1997-03-28  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Patentin Ver. 2.0





Db 1413 CAAGGGCTATACCAAGTCCATCGACATCTGGTCTGTGGGCTGCATTTCTGGCTGAGATGCT 1472  
QY 770 CAACCGCCAGCCGCTCTTCCCGGCGAGGACACATGCAACAGATGGCGCTCATCACCGA 829  
Db 1473 CTCTAACCGGCCCATCTTCCCTGGCAAGCACTACTGGATCAGTCAACCACTTTGGG 1532  
QY 830 GGTGATCGGAGCCCGGAGCGAGCAGCAGAGCTGGGGTTCAACGGAACGAGAGCCGAGGAA 889  
Db 1533 CATCTGGGCTCCCATCTCCAGGAGGACCTGAATTTGTATCATCAACATGAAGGCCGAAA 1592  
QY 890 GTACATGAGCACTGCGCAGTACCGCGCCGAGGTTGCGGAGCATGTTCCCGGGGT 949  
Db 1593 CTACCTACAGTCTTGCCCTTCCAGACCAAGTGGCTTGGGCCCAAGCTTTTCCCAAGTC 1652  
QY 950 GCACCGCCGCGCTCGACCTCATCGAGAGATGCTCACCTTCAACCGCTGCAGAGAAAT 1009  
Db 1653 AGACTCCAAAGCCCTTGACCTGTGACCGGATGTTAACTTTAAACCCCAATPAACGGAT 1712  
QY 1010 CACAGTTGAGGAGCGCTCGATCATCTTACCTAGAGAGATTGCAAGACATGCCGATGA 1069  
Db 1713 CACAGTGGAGGAGCGCTGGCTCACCCCTACCTGAGCAGTACTATGACCCGACGATGA 1772  
QY 1070 GCCCATCTGCTGAGGCCCTTCTCTTCCGACTTGGAGGAGGCTTAAACGAGGACCA 1129  
Db 1773 GCCAGTGGCGAGGAGCCCTTACCTTGGCCATGGAGTGGATGACCTACCTTAAGGAGCG 1832  
QY 1130 AATGAAGCAGCTGATCTTCAACGA 1153  
Db 1833 GCTGAAGGAGCTCATCTTCCAGGA 1856

## RESULT 7

US-09-417-197-56  
; Sequence 56, Application US/09417197  
; Patent No. 6518021  
; GENERAL INFORMATION:  
; APPLICANT: Ole THASTRUP, et al.  
; TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An  
; FILE REFERENCE: 3759-0110P  
; CURRENT APPLICATION NUMBER: US/09/417,197  
; CURRENT FILING DATE: 1999-10-07  
; NUMBER OF SEQ ID NOS: 143  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 56  
; LENGTH: 1875  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: mERK1-F64L-S65T-GFP fusion  
; NAME/KEY: CDS  
; LOCATION: (1)..(1872)  
US-09-417-197-56

Query Match 23.9%; Score 334; DB 3; Length 1875;  
Best Local Similarity 61.1%; Pred. No. 5.7e-64;  
Matches 601; Conservative 0; Mismatches 365; Indels 18; Gaps 3;

QY 182 CACGCGCCCATCATGCCCATTGGCGCGGCTACGGGATCGTCTGCTCCGTGATGAA 241  
Db 126 CTACACGCACTGCAGTACATCGCGGCGGTACGGCATGTGTCAGCTCATGATGA 185  
QY 242 CTTTGTAGACAGGAGATGTTGGCGATAAAGAGATCGCCACGCGTTCAACACACAT 301  
Db 186 CCAGTGGCGAAGACCAAGAGTGGCCATCAAGAGAT---CAGCCCTTTGAGGATCAAC 242  
QY 302 GAGCGCAAGCGCACGCTCCGGAGATCAAGCTCTCAGCACCTGACCAAGAGACAT 361  
Db 243 CTACTGTGAGCGCAAGCTGAGGAGATCCAGATCTTGTGCGATTCCGCGCATGAGATGT 302  
QY 362 CATAGGCATCAGGGATGTGATCCGCGCGGATCCCTCAGGCGGTTCAACGAGCTCTACAT 421

Db 303 TATAGGCATCCGAGACATCTCTCAGAGCGCCACCTCGAAGCCATGAGAGATGTTTACAT 362  
QY 422 CGCCACGAGAGCTCATGAGCACCGAGCTCCATCACATCATCCGCTCCAAACAAGAACTGTC 481  
Db 363 TGTTCAGGACCTCATGAGAGACAGACT---GTACAAGCTGCTTAAAGCCAGCAGCTGAG 419  
QY 482 AGAAGAGCACTGCCAGTATTTCTGTACAGATCTTGGGGGGCTCAAGTATCATCATCTC 541  
Db 420 CAATGACCACTCTGCTACTTCTCTATCCAGATCTCCGGGGCTCAAGTATATACATCTC 479  
QY 542 GCGAAGCTGATCCACCGGAGCTCAAGCGAGCAACCTGCTGCTGACGCGCAACTGCGCA 601  
Db 480 AGCCAAATGTGCTGCAACCGGAGCTTGAAGCTTTCCAATCTGCTTATCAACACCACTGCGA 539  
QY 602 CCTCAAGATCTCGACTTTCGGGCTGGCGG-----CGTCTGCGAGAGCGA 649  
Db 540 CTTTAAGATCTGTGATTTTGGCTTGGCCCGGATTGCTGACCTGAGCAGCACCACACTGG 599  
QY 650 CATGATGACGAGTACGTGGTCAACCGGTGGTACCGCGCGGAGCTGCTCTCAACTC 709  
Db 600 CTTTCTGACGAGTATGTGGCCACACGCTGTGTACCGAGCCCGAGAGATCATGCTTAATTC 659  
QY 710 CACGCACTACTCGCGCGCATCGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 769  
Db 660 CAAGGGCTACACCAATCCATCGACATCTGGTCTGTGGGCTGCAATTTGGCTGAGATGCT 719  
QY 770 CAACCGCGCAGCGCTCTTCCCGGAGGAGCACATGACACAGATGCGGCTCATCACCGA 829  
Db 720 CTCGAACCGGCCATCTTCCCGGCAAGCATCTACCTGGACCACTCAACCATTTCTAGG 779  
QY 830 GGTGATCGGAGCCGAGCAGCAGAGCTGGGGTTTACAGAAACGAGGAGCGAGGAA 889  
Db 780 TATCTTGGGTTCCCCATCCGAGGAGACTTAATTTGCATCATTAACATGAAGGCCCGAAA 839  
QY 890 GTACATGAGGACCTGCGCGAGTACCGCGCGGAGCTTCGCGAGCATGTTCCCGGGGT 949  
Db 840 CTACCTGAGTCTCTGCGCTCGAAACCAAGTGGCTTGGGCAAGCTCTTTCTTAAATC 899  
QY 950 CGAGCGCGCGCTCGACCTCATCGAGAGATGCTCACTTCAACCGCTGCGAGAGAT 1009  
Db 900 TGACTCCAAAGCTCTTGACCTGCTGGAACGGATTTAACTTCAACCCCAACAGCGCAT 959  
QY 1010 CACAGTTGAGGAGCGCTCGATCATCTTACAGAGATTTGACGAGCATCGCGATGA 1069  
Db 960 CACAGTAGAGGAAAGCGCTGGCTCACCTTACCTGGAACAGTACTAGCATCCGACAGATGA 1019  
QY 1070 GCCCATCTGCTGAGCGCTTCTCTTCCGACTTTCGAGCAGAGGCTCTAAACGAGGACCA 1129  
Db 1020 GCCAGTGGCGGAGGAGCCATTCACCTTCGACATGAGTGGATGACCTCCCAAGGAGCG 1079  
QY 1130 AATGAAGCAGCTGATCTTCAACGA 1153  
Db 1080 GCTGAAGGAGTGTATCTTCCAGGA 1103

## RESULT 8

US-09-828-313-8/c  
; Sequence 8, Application US/09828313  
; Patent No. 6867351  
; GENERAL INFORMATION:  
; APPLICANT: COSTA e SILVA, OSWALDO DA  
; APPLICANT: BOHNERT, HANS J.  
; APPLICANT: THIELEN, NOCHA VAN  
; APPLICANT: CHEN, RUYING  
; APPLICANT: SARRIA-MILLAN, RODRIGO  
; TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED PROTEINS AND METHODS OF  
; FILE REFERENCE: 16313-0032  
; CURRENT APPLICATION NUMBER: US/09/828,313  
; CURRENT FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/196,001  
; PRIOR FILING DATE: 2000-04-07







CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pennie & Edmonds  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10036-2711  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/458,887  
 FILING DATE: 02-JUN-1995  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/701,544  
 FILING DATE: 16-MAY-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Miarock, S. Leslie  
 REGISTRATION NUMBER: 18,872  
 REFERENCE/DOCKET NUMBER: 6526-049  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212 790-9090  
 TELEFAX: 212 869-8864/9741  
 TELEX: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1747 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: unknown  
 MOLECULE TYPE: DNA (genomic)  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..1095  
 US-08-458-887-1

Query Match 22.8%; Score 318; DB 2; Length 1747;  
 Best Local Similarity 60.1%; Pred. No. 1.9e-60;  
 Matches 591; Conservative 0; Mismatches 375; Indels 18; Gaps 3;

QY	182	CCAGCGCCCATCATGCCATTCGCGCGCGCTACGGGATCGTCTGCTCCGCTGATGAA	241
DB	81	CTACAGCGACTGCAGTACATCGCGGCGGCTACGGCATGCTCAGCTCAGCATATGA	140
QY	242	CTTTGAGACGAGGAGATGTTGGCGATTAAGAAGATCGCCAAACGCGTTCAACACGACAT	301
DB	141	CCACGTGCGCAAGACACAGATGCTATCAAGAAGAT---CAGCCCTTCGAGCATCAAAAC	197
QY	302	GGACGCCACGCGACCGCTCGGCGGATCAAGCTCCTCAGCAGCTCGACACGACAT	361
DB	198	CTACTGTGACGCGACCGCTGAGGAAATCCAGATCTTGTGCGGATTCGCGCATGAGATGT	257
QY	362	CATAGGATCAGGATGTTGATCCGCGCGGATCCCTCAGCGCGTTCAACGCGCTTACAT	421
DB	258	CATAGGATCCGAGACATCTCAGACACCCCTCGGAAGCCATGAGATGTTTACAT	317
QY	422	CGCCACGAGCTCATGGACACCGACCTCCATCATCATCCGCTCCAAACCAAGAACTGTC	481
DB	318	TGTTGAGGACTCATGGAGCGGACCT---GTACAAGCTGCTAAAGAGCCAGCAGCTGAG	374
QY	482	AGAAGACACTGCCAGTATTTCTGTACAGATCCTCGGGGCTCAAGTACATCCACTC	541
DB	375	CAATGACCATCTGCTACTTCTCTACAGATCCTCCGGGGCTCAAGTACATACACTC	434
QY	542	GGGGAACGTGATCCACCGCGACCTGAAAGCGGAGCAACCTGCTGCTGAACGCCAACTGCGA	601
DB	435	GGCAATGTCTGCACCGCGGACCTGAAGCCCTCCATCTGCTTATCAACACCACTTGGGA	494
QY	602	CCTCAAGATCTGGACTTCGGGCTGGCGCGG-----CCGTCGTCGAGAGCGGA	649

DB	495	CCTAAGATCTGTGATTTTGGCTTGGCGGATGCTGACCTGAGACGACACACTGG	554
QY	650	CATGATACGGAGTACGTGGTCAACCGGTGTACCGCGCGCGGAGCTGCTCTCAACTC	709
DB	555	CTTTCTGACCGAGTATGTGGCCACACGCTGGTACGAGCCCGAGAGATCATGCTTAACTC	614
QY	710	CACCGACTACTCCCGCCCATGAGCTGTGGTCCGCTGCGCTGATCTTCAAGAGTCAAT	769
DB	615	CAAGGGCTACACCAAAATCAATGACATCTGGTCTGTGGGCTGCAATCTGGCTGAGATGT	674
QY	770	CAACCGCCAGCGCTCTTCCCGCGGAGGACCAACATGACACGATGCGCTCATCACCGA	829
DB	675	CTCCAAACCGGCTATCTTCCCGCGCAAGCACTTACCTGGACCAAGCTCAACCAATCTAGG	734
QY	830	GCTGATCGGAGCGCGACGAGCTGGGGTTTATACGGAACGAGGAGCGCGAGAA	889
DB	735	TATCTGGGTTCCCATCCAGAGGACCTAAATTTGATATTAACATGAAGGCCCGAAA	794
QY	890	GTACATGAGGACCTGCGCGCAGTACCCGCGCGGAGCTTTCGCGAGCATGTTCCCGGGT	949
DB	795	CTACCTACAGTCTCTGCGCTCTTAAACCAAGGTGGCTTTGGGCAAGCTTTTCCCAATC	854
QY	950	GCAGCGCGCGGCTCGACCTCATCGAGAGATGCTCACCCTCAACCCGCTCGAGAGAT	1009
DB	855	TGACTCCAAAGCTCTTGACCTGCTGACCGGATGTTAAACCTTTAAACCCCAACAAAGCGAT	914
QY	1010	CACAGTTGAGGAGCGCTCGATCATCTTACCTAGAGAGATGTCAGACATGCCGATGA	1069
DB	915	CACAGTAGAGGAGCACTGGCTCACCCTTACCTGGAACAGTACTATGATCCGACAGATGA	974
QY	1070	GCCCATCTGCTGGAGCCCTTCTCTTCGACTTCGAGCAGAAAGGCTCTAAACGAGAGCA	1129
DB	975	ACCAGTGGCTGAGGAGCCATTCACCTTTGACATGAGCTGGATGATCTCCCCAAGAGCG	1034
QY	1130	AATGAAGCAGCTGATCTTCAACGA	1153
DB	1035	GCTGAAGGAGCTGATCTTCCAAGA	1058

RESULT 13  
 US-08-932-787B-1  
 ; Sequence 1, Application US/08932787B  
 ; Patent No. 6277963  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Boulton et al.  
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TOWARD EXTRACELLULAR SIGNAL-RELATED  
 ; TITLE OF INVENTION: KINASES  
 ; FILE REFERENCE: REG 430-A-1  
 ; CURRENT APPLICATION NUMBER: US/08/932,787B  
 ; PRIOR FILING DATE: 1997-09-18  
 ; PRIOR APPLICATION NUMBER: 08/469,547  
 ; PRIOR FILING DATE: 1995-06-06  
 ; PRIOR APPLICATION NUMBER: 08/178,488  
 ; PRIOR FILING DATE: 1994-01-07  
 ; PRIOR APPLICATION NUMBER: 07/701,544  
 ; PRIOR FILING DATE: 1991-05-16  
 ; PRIOR APPLICATION NUMBER: 07/532,004  
 ; PRIOR FILING DATE: 1990-06-01  
 ; NUMBER OF SEQ ID NOS: 21  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 1  
 ; LENGTH: 1747  
 ; TYPE: DNA  
 ; ORGANISM: RAT  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)...(1095)  
 ; OTHER INFORMATION: ERK1 cDNA  
 US-08-932-787B-1

Query Match 22.8%; Score 318; DB 3; Length 1747;  
 Best Local Similarity 60.1%; Pred. No. 1.9e-60;  
 Matches 591; Conservative 0; Mismatches 375; Indels 18; Gaps 3;



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QY 182 CAGCGCCCATCATGCGCCATTGCGCGCGCGCTACGGGATCGTCTGCTCCGTGATGAA 241
Db 81 CTACACGAGCTGACGATACATCGCGGAGCGCGTACGGCATGTCAGCTCAGCATATGA 140
QY 242 CTTTGTAGAGAGGAGATGCTGCGGATAAAGAGATCGCCACGCGTTCAACAACGACAT 301
Db 141 CACGCTGCGGACAGAGTGGCTTATCAAGAGAT---CAGCCCTTCGAGCATCAAC 197
QY 302 GAGCGCAAGCGCACGCTCGGGAGATCAAGCTCCTCAGGCACCTCGACACGAGAACAT 361
Db 198 CTACTGTGACGCGCACGCTGAGAGAAATCCAGATCTTGTCTCGGATTCGGCCATGAGATGT 257
QY 362 CATAGGATCAGGATGTGATCCCGCGCGGATCCCTCAGGCGTTCAAAGAGCTTACAT 421
Db 258 CATAGGATCCGAGACATCTCAGAGCACCACCTCGGAGCCATGAGAGATGTTTACAT 317
QY 422 CGCCACGAGCTCATGAGACCGGCTCCATCATCATCGCTCCAAACCAAGAACTGTC 481
Db 318 TGTTGAGGACCTCATGAGACCGGCT---GTAAAGCTCTAAAGAGCCGAGCTGAG 374
QY 482 AGAAGAGCACTGCGAGTATTTCTGTACAGATCTCGCGGGGCTCAAGTACATCCACTC 541
Db 375 CAATGACCATCTGCTACTTCTCTACAGATCTCGGGGCTCAGGTACATACACTC 434
QY 542 GCGGAACTGATCCACGCGACCTGAGGCGAGCAACTGCTGCTGTAACCGCAACTGCGGA 601
Db 435 GGCCTATGCTGACCGGAGCTGAGGCGCTGAAAGCTTCAATCTGCTTATCAACACCACTCGGA 494
QY 602 CCTCAAGATCGGATCTGCGGCTGCGGCGG-----CCGCTCGTGGAGGCGA 649
Db 495 CCTTAAGATCTGATTTTGGCCCTTGGCGGATGCTGACCTTAAGAGCCGAGCTGAG 554
QY 650 CATGATGAGGAGTACGCTGCTGACCGGCTGAGTACCGCGCGCGGAGCTGCTGCTCAACTC 709
Db 555 CTTTCTGACCGAGTATGTGGCCACACGCTGTTACCGAGCCCGAGAGATATGCTTAATC 614
QY 710 CACCGACTACTCCCGCGCCATCGACGCTGCTGGTCCGCTGCTGATCTTCAATGAGGCTCAT 769
Db 615 CAAGGGCTACACCAAAATCCATGACATCTGCTGCTGGGCTGCAATCTGGCTGAGATGCT 674
QY 770 CAACCGCGAGCGCTCTTCCCGCGAGGACCAATCATGACAGTGGCTCATCACCGA 829
Db 675 CTCACCGGCTATCTTCCCGCGAGCACTACCTGGAACGCTCAACCAATCTTAGG 734
QY 830 GGTGATCGGACGCGGACGAGCTGAGCTGGGGTTCTACGGAACGAGGACGCGAGGAA 889
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QY 890 GTACATGAGGACCTGCGGAGTACCGCGCGCGGAGCGTTCCGAGCATGTTCCGCGGGT 949
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QY 950 GCGAGCGCGCGCTGACCTCATCGAGAGAGTCTCACCCTTCAACCGCTGAGAGAT 1009
Db 855 TGACTCCAAAGCTCTTGACCTGCTGAGCCGAGTGTAAACCTTTAAACCAACCAAGCGCAT 914
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Db 915 CACAGTAGAGAGCACTGGCTCACCCTTACCTGGAACAGTACTATGATCGGACAGATGA 974
QY 1070 GCCCATCTGCTGGAGCGCTTCTCTTCCGATTCGAGCAGAGGCTCTAAACGAGGACCA 1129
Db 975 ACCAGTGGCTGAGGAGCAATTACCTTTGACATGGAGCTGGATGATCTCCCAAGGAGCG 1034
QY 1130 AATGAACAGCTGATCTTCAAGCA 1153
Db 1035 GCTGAAGGAGCTGATCTTCAAGA 1058
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RESULT 14

US-08-932-012C-1

; Sequence 1, Application US/08932012C

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; Patent No. 6297035
; GENERAL INFORMATION:
; APPLICANT: Boulton et al.
; TITLE OF INVENTION: A FAMILY OF MAP2 PROTEIN KINASES
; FILE REFERENCE: REG 430-Y-1
; CURRENT APPLICATION NUMBER: US/08/932,012C
; CURRENT FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 08/462,874
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: 08/178,488
; PRIOR FILING DATE: 1994-01-07
; PRIOR APPLICATION NUMBER: 07/701,544
; PRIOR FILING DATE: 1991-05-16
; PRIOR APPLICATION NUMBER: 07/532,004
; PRIOR FILING DATE: 1990-06-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1747
; TYPE: DNA
; ORGANISM: RAT
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1095)
; OTHER INFORMATION: ERK1 cDNA
; US-08-932-012C-1
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Query Match 22.8%; Score 318; DB 3; Length 1747;

Best Local Similarity 60.1%; Pred. No. 1.9e-60;

Matches 591; Conservative 0; Mismatches 375; Indels 18; Gaps 3;

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QY 182 CMAGCGCCCATCATGCGCGCGCGCTACGGGATCGTCTGCTCCGTGATGAA 241
Db 81 CTACACGAGCTGACGATACATCGCGGAGCGCGTACGGCATGTCAGCTCAGCATATGA 140
QY 242 CTTTGTAGAGAGGAGATGCTGCGGATAAAGAGATCGCCACGCGTTCAACAACGACAT 301
Db 141 CACGCTGCGGACAGAGTGGCTTATCAAGAGAT---CAGCCCTTCGAGCATCAAC 197
QY 302 GAGCGCAAGCGCACGCTCGGGAGATCAAGCTCCTCAGGCACCTCGACACGAGAACAT 361
Db 198 CTACTGTGACGCGCACGCTGAGAGAAATCCAGATCTTGTCTCGGATTCGGCCATGAGATGT 257
QY 362 CATAGGATCAGGAGTGTGATCCCGCGCGGATCCCTCAGGCGTTCAAAGAGCTTACAT 421
Db 258 CATAGGATCCGAGACATCTCAGAGCACCACCTCGGAGCCATGAGAGATGTTTACAT 317
QY 422 CGCCACGAGCTCATGAGACCGGCTCCATCATCATCGCTCCAAACCAAGAACTGTC 481
Db 318 TGTTGAGGACCTCATGAGACCGGCT---GTAAAGCTCTAAAGAGCCGAGCTGAG 374
QY 482 AGAAGAGCACTGCGAGTATTTCTGTACAGATCTCGCGGGGCTCAAGTACATCCACTC 541
Db 375 CAATGACCATCTGCTACTTCTCTACAGATCTCGGGGCTCAGGTACATACACTC 434
QY 542 GCGGAACTGATCCACGCGACCTGAGGCGAGCAACTGCTGCTGTAACCGCAACTGCGGA 601
Db 435 GGCCTATGCTGACCGGAGCTGAGGCGCTGAAAGCTTCAATCTGCTTATCAACACCACTCGGA 494
QY 602 CCTCAAGATCGGATCTGCGGCTGCGGCGG-----CCGCTCGTGGAGGCGA 649
Db 495 CCTTAAGATCTGATTTTGGCCCTTGGCGGATGCTGACCTTAAGAGCCGAGCTGAG 554
QY 650 CATGATGAGGAGTACGCTGCTGACCGGCTGAGTACCGCGCGCGGAGCTGCTGCTCAACTC 709
Db 555 CTTTCTGACCGAGTATGTGGCCACACGCTGTTACCGAGCCCGAGAGATATGCTTAATC 614
QY 710 CACCGACTACTCCCGCGCCATCGACGCTGCTGGTCCGCTGCTGATCTTCAATGAGGCTCAT 769
Db 615 CAAGGGCTACACCAAAATCCATGACATCTGCTGCTGGGCTGCAATCTGGCTGAGATGCT 674
QY 770 CAACCGCGAGCGCTCTTCCCGCGAGGACCAATCATGACAGTGGCTCATCACCGA 829
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Db 675 CTCAAACCGGCTATCTTCCCGGCAAGCACTACCTGGACCAGCTCAACCAATTTCTAGG 734  
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Db 735 TATACCTGGGTTCCCATCCCAAGAGGACCTAAATTTGATCATTAACATGAGGCGCCGAAA 794  
Qy 890 GTACATGAGGCACCTGCGGAGTACCCTGGGCGGAGCTTCGCGAGCATGTTCCCGGGGT 949  
Db 795 CTACCTACAGTCTCTGCCCTCTAAACCAAGGTGGCTTGGGCCAAGCTTTTCCCAATC 854  
Qy 950 GAGCGCGCGCGCTCGACCTCATCGAGAGGATGCTCACTTCAACCCGCTGCGAGAAAT 1009  
Db 855 TGACTCCAAAGCTCTTGACCTGCTGGACCGGATGTTAACTTTAAACCCAAACAAAGGCGAT 914  
Qy 1010 CACAGTTGAGGAGCGCTCGATCATCTTACCTTAGAGAGATTGCGAGCATGCGCGATGA 1069  
Db 915 CACAGTAGAGGAGGAGCTGGCTCACCTTTACCTTGGAAAGTACTATGATCCGACATGA 974  
Qy 1070 GCCCATCTGCTGGAGCGCTTCTCTTCGACTTCGAGCAGAAGGCTCTAAACGAGGACCA 1129  
Db 975 ACCAGTGGCTGAGGAGCCATTACCTTTGACATGGAGCTGGATGATCTCCCCAAGGAGCG 1034  
Qy 1130 AATGAAGCAGCTGATCTTCAACGA 1153  
Db 1035 GCTGAAGGAGCTGATCTTCCAAGA 1058

## RESULT 15

US-08-888-818C-1  
; Sequence 1, Application US/08888818C  
; Patent No. 6303358  
; GENERAL INFORMATION:  
; APPLICANT: Boulton et al.  
; TITLE OF INVENTION: A FAMILY OF MAP2 PROTEIN KINASES  
; FILE REFERENCE: REG 430-V-1  
; CURRENT APPLICATION NUMBER: US/08/888,818C  
; PRIOR FILING DATE: 1997-07-07  
; PRIOR APPLICATION NUMBER: 08/478,985  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 08/178,488  
; PRIOR FILING DATE: 1994-01-07  
; PRIOR APPLICATION NUMBER: 07/701,544  
; PRIOR FILING DATE: 1991-05-16  
; PRIOR APPLICATION NUMBER: 07/532,004  
; PRIOR FILING DATE: 1990-06-01  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 1747  
; TYPE: DNA  
; ORGANISM: RAT  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1095)  
; OTHER INFORMATION: ERK1 cDNA  
US-08-888-818C-1

Query Match 22.8%; Score 318; DB 3; Length 1747;  
Best Local Similarity 60.1%; Pred. No. 1.9e-60;  
Matches 591; Conservative 0; Mismatches 375; Indels 18; Gaps 3;  
Qy 182 CCAGCGCCCATCATGCCCCATTTGGCGCGCGCTACGGGATCGTCTGCTCCGATGATGA 241  
Db 81 CTACAGCAGCTGCAGTACATCGCGGAGGCGGCTAGGCGTGTGCTCAGCTCAGCATATGA 140  
Qy 242 CTTTGTAGACAGGGAGATGTTGGCGATTAAGAGATGCGCAACGCGTTCAACACGACAT 301  
Db 141 CCAGCTGCGCAAGACCAAGTGGCTATCAAGAAGAT---CAGCCCCCTTCGAGCATCAAAC 197  
Qy 302 GGAGCGCAAGCGGACGCTCCGGGAGATCAAGCTCCTCAGGCACCTCGACCACGAGACAT 361  
Db 198 CTACTGTACGCGCACGCTGAGAGAAATCCAGATCTTGTCTCGGATTCGCGCATGAGAAATGT 257

Qy 362 CATAGGSCATCAGGGATGTGATCCCGCGCCGATCCCTCAGGCGTTCAACGACGTCTACAT 421  
Db 258 CATAGSCATCGAGACATCTCTCAGAGCACCCACCTCGAAGCCATGAGAGATGTTTACAT 317  
Qy 422 CGCCACGAGCTCATGGACACGAGCTCCATCAGATATCCGCTCCAACCAAGAAGTGTCT 481  
Db 318 TGTTCAGGACCTCATGGAGACGAGCT---GTAAAGCTGTAAAGAGCAGCAGCTGAG 374  
Qy 482 AGAAGACACTGCGAGTATTTCTGTACAGATCTCGGGGGCTCAAGTATACATCACATC 541  
Db 375 CAATGACCACTCTGCTACTTCTCTACAGATCTCTCGGGGCTCAGTATACATACATC 434  
Qy 542 GCGAACCTGTGATCCACCGGACCTGAAGCCGAGCAACTGCTGTGAACGCCAATGCGA 601  
Db 435 GGCCTAATGTGTGTCACCGGACCTGAAGCCCTCCAATCTGCTTATCAACACCACTGCGA 494  
Qy 602 CCTAAGATCTCGGACTTTCGGGCTCGCGGG-----CGTCTCGGAGGCGA 649  
Db 495 CTTAAGATCTGTGATTTTGGCTTTGCCGGATTGCTGACCTGAGCAGCAGCACACTGG 554  
Qy 650 CATGATGAGGAGTACGTGGTCACCCGGTGGTACCGCGCGCGGAGCTGCTGCTCAACTC 709  
Db 555 CTTTCTGACCGGATATGTGGCCACACGCTGGTACCGAGCCCGAGAGATCATGCTTAATC 614  
Qy 710 CACCGACTACTCCGCGCCATCGAGCTCTGGTCCGTGCGCTGCACTTTTCATGGAGCTCAT 769  
Db 615 CAAGGGCTACACCAAAATCCATTGACATCTGGTCTGTGGGCTGCACTTCTGGCTGAGATGCT 674  
Qy 770 CAACCGCAGCGCTCTTCCCGGAGGAGCACATGCAACGAGATGCGGCTCATCACCGA 829  
Db 675 CTCCAACCGGCTATCTTCCCGGCAAGCACTACCTGGACCAGCTCAACCAATTTCTAGG 734  
Qy 830 GGTGATCGGACGCGGAGCGAGCTGGGTTTCATACGGAACGAGGAGCGCGAGAA 889  
Db 735 TATACTGGGTTCCCATCCAAAGAGACCTAAATTTGATCATTAACATGAAGGCCCGAAA 794  
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Qy 1070 GCCCATCTGCTGGAGCGCTTCTCTTCGACTTCGAGCAGAAGGCTCTAAACGAGGACCA 1129  
Db 975 ACCAGTGGCTGAGGAGCCATTCACTTTGACATGGAGCTGGATGATCTCCCCAAGGAGCG 1034  
Qy 1130 AATGAAGCAGCTGATCTTCAACGA 1153  
Db 1035 GCTGAAGGAGCTGATCTTCCAAGA 1058

Search completed: December 29, 2005, 07:49:10  
Job time : 206 secs









[illegible]

## RESULT 6

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US-10-425-114-3164
; Sequence 3164, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kowalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313) B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 3164
; LENGTH: 873
; TYPE: DNA
; ORGANISM: Zea mays

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; FEATURE:									
; OTHER INFORMATION: Clone ID: 700242603_FLI									
US-10-425-114-3164									
Query Match 38.9%; Score 543; DB 7; Length 873;									
Best Local Similarity 89.3%; Pred. No. 1.2e-147;									
Matches 585; Conservative 0; Mismatches 70; Indels 0; Gaps 0;									
Qy	537	CACTCGCGCAACG	TGATCC	ACCGCGACTG	AAAGCCGAGCA	ACCTGCTG	CTGAACGCCAAC	596	
Db	1	CAC	TCCGCCAACG	TGATCC	ACCGCGACTC	AAAGCCGAGCA	ACCTGCTG	CTGAACGCCAAC	60
Qy	597	TGCGACCTCA	AGATCTCG	AGCTTTCGG	CGTGGCGGCGCGCT	CGTCGGAGCGG	CATCATG	656	
Db	61	TGCGACCTCA	AGATCTCG	AGCTTTCGG	CGTGGCGGCGCGCT	CGTCGGAGCGG	CATCATG	120	
Qy	657	ACGGAGTAC	GTGGTG	CACCCGGTGT	ACCGCGCGCGGAGCT	TGCTGCTCA	ACTCCACCGC	716	
Db	121	ACGGAGTAC	GTGGTG	CAACCGCTG	TACTACCGCGCGCGGAGCT	TGCTGCTCA	ACTCCACCGC	180	
Qy	717	TACTTCGCG	CCCATCG	AGCTCTGGT	CCGTGGCTG	CATCTTCAT	TGGAGCTCAT	776	
Db	181	TACTTCGCG	CCCATCG	AGCTCTGGT	CCGTGGCTG	CATCTTCAT	TGGAGCTCAT	240	
Qy	777	CAGCGCTCT	TCCCGCAG	GGACCA	CATGCA	CCAGATG	CGCCTCAT	836	
Db	241	CAGCGCTCT	TCCCGCAG	CGACCA	CATGCA	CCAGATG	CGCCTCAT	300	
Qy	837	GGGACGCG	ACGACG	AGAGCTGG	GGGTTC	ATACGGAA	CGAGGACG	896	
Db	301	GGGACGCG	ACGACG	AGATGAGCT	CGGGTT	CATCCGGAA	CGAGGACG	360	
Qy	897	AGGCACTTC	GCGCAGT	ACCGCG	CCGACGTTTCG	CGAGCATGTT	CCCGCGGGT	956	
Db	361	CGCCACTTC	CGCAGTTCC	CGCGCGCGCGT	TGTCAG	CGCTGTTTCC	CGCGATCG	420	
Qy	957	GCGCGCTG	CACTCAT	TCGAGAG	ATGCTCA	CTTTCA	ACCCGCTG	1016	
Db	421	GTCGCGT	TGGACCTCAT	TCGAGCG	ATGCTCA	CTTTCA	ACCCGCTG	480	
Qy	1017	GAGGAGCG	CTCGATCAT	CTCTTACT	AGAGAGATTG	CA	CGACATCG	1076	
Db	481	GAAGAGCG	CTTGGAGCA	CCCGTACT	CTGGAA	ACGGGTACA	CAGACGTG	540	
Qy	1077	TGCCCTGGA	GCCTTCTCT	CTTCGACTT	CGAGCAGA	AGGCTCTTAA	ACGAGGAC	1136	
Db	541	TGCACGGA	CCCGTCTCT	CTGTCGACTT	CGAGCAG	CAGGCTCTG	CA	600	
Qy	1137	CAGCTGAT	CTTTCAA	CGAAGCG	ATCGAGAT	GAACCCAA	CAATCCGGT	1191	
Db	601	CAGCTGAT	CTTTCAA	CGAGGGCAT	CGAACTCG	AACTCCGCA	CTTCCGAT	655	

## RESULT 7

US-09-938-842A-644  
; Sequence 644, Application US/09938842A  
; Patent No. US20020160378A1  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; TITLE OF INVENTION: SAME, AND METHODS OF USE  
; FILE REFERENCE: SCRIPT300-3  
; CURRENT APPLICATION NUMBER: US/09/938,842A  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/300,111  
; PRIOR FILING DATE: 2001-06-22



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; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 644
; LENGTH: 1188
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-644

Query Match          36.4%; Score 508.8; DB 3; Length 1188;
Best Local Similarity 67.2%; Pred. No. 1.3e-137;
Matches 736; Conservative 0; Mismatches 357; Indels 3; Gaps 1;

QY  92  GGTGGCGGAGTTTCAGCGCGAGATGACGCGCGGATGACGCGCGGCTACCTCTACGACATCTT 151
DB  96  GATTGAGAAATATTCGCGCGACTCTTAGCCATGTTGGTGTATTTATTCAGTATAACATATT 155

QY  152  CGGGAACAAGTTTCGAGGTGACGAAACAAGTACCAAGCCGCCCATCATGCCCATTTGGCGCGG 211
DB  156  TGGAAACATCTTCGAGGTCAACCGCTAAGTATAAGCTCCGATCATGCTTATTTGGCAAGGG 215

QY  212  CGCTACGGGATCGTCTGCTCGTGATGAACTTTTGAGACGAGGAGATGTTGGCGGATAAA 271
DB  216  TGCTTATGGCATCGTTTGTTCGGCTATGAATCTGAAACTTAACGAGAGCGTTGCGATTAA 275

QY  272  GAAGATCGCAACGCTTCAACACGACATGAGCGCAAGCCAGCGCAGCTCGGGAGATCAA 331
DB  276  GAAATTTGCTAACGCTTTTGACAAATGAATGATGATTAAGAGGACTCTCGTGAGATCAA 335

QY  332  GCTCTCAGGACCTCGACCGGATGACGAAACATCATAGGCATCAGGGATGTGATCCCGCGCC 391
DB  336  GCTGCTTCGTCACATGATGATAAATATTTGTCATCAGAGATATTATCCCGCCACC 395

QY  392  GATCCCTCAGGCGTTCAACGAGTCTACATTCGCCACGAGCTCATGGAACCGACCTCCA 451
DB  396  ATTAAGAAACGCTTTCAACGATGTTTACATTCGGTATGAGTTAAATGGACACTGATCTCCA 455

QY  452  TCACATCATCGCTCCAAACGAACTGTCCAGAGGACACTGCCAGTATTTCTGTACCA 511
DB  456  TCAATATCATTCGGTCAAAATCAAGCATTTACCGAAGAACATTTGCCAGTATTTCTTTACCA 515

QY  512  GATCTCTCGGGGCTCAAGTACATCCACTCGGCGAAGCTGATCCACCGGACCTGAAGCC 571
DB  516  GATCCCTCGGTGATTGAAATACATTCATCTGCAATATGCTTCACAGGAGTTTGAACC 575

QY  572  GAGCAACCTGCTGCTGAAACGCAACTTCGAGCTTCAAGATCTGCGACTTCGGGCTGGCGG 631
DB  576  AAGTAATCTCTCTCGAAGCGCAACTTCGCACTTAAATACTGCGATTTTGGGCTAGCTCG 635

QY  632  GCGTCTCGGAGAGGACATGATGACGGAGTACGTGTTCAACCGGTGGTACCGCGCGC 691
DB  636  AGTCACCTTCGAGAGTATTTCAATGACTGAATATGTTGTCAGAGATGGTACCGTGACAC 695

QY  692  GGAGCTGCTGCTCAACTCCACCGACTACTCCGCGCGCATCGAGCTCTGGTCTCGGCTG 751
DB  696  AGAGCTTCTTTAAATCTTCTGATTAATCTGAGCTATCGATGTTTGGTCTGTAGGCTG 755

QY  752  CATCTTCAAGAGCTCATCAACCGCGAGCGCTCTTTCCCGGAGGAGGACACATGACCA 811
DB  756  TATTTTCATGGAGTTAATGAGCGTAAGCCACTCTTTCCCTGGACGAGATCATGTCCATCA 815

QY  812  GATGCGCTCATCACCGAGGTGATCGGGAGCGCGAGGACGAGCTGGGTTTCATAG 871
DB  816  GCTTCGCTTGTCTATGAGGCTCATAGGAATCTCCATCAGAGAAGAGCTCGAGTTCTT--- 872

QY  872  GAAACGAGGACCGGAGGAAGTACATGAGGCACTTCGCCGAGTACCCCGCGCGGACGTTCCG 931
DB  873  GAAACGAAACGCAAGGATACATAGACAGCTTCCACCTTATCTCTCGCAATCCATCAC 932

QY  932  GAGCATGTTCCCGCGGTTGAGCGCCCGCGCTTCGACCTCATCGAGAGAGTGTCACTTT 991
DB  933  TGAATAAGTTTCCCGACAGTGTCTTTTAGCTATAGACCTTATCGAGAAGATGTTAACT 992

QY  992  CAACCGCTGCAGAGATCACAGTTTCAGGAGGCGCTCGATCATCTTCTTACCTAGAGATT 1051
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DB  993  TGATCTAGACGGAGAAATCACAGTTTTTTAGACGCATTTGGCCCATCCATACCTGAATCGTT 1052
QY  1052  GCACGACATCGCCGATGAGCCCATCTGCTCGAGCCCTTCTCTTCGACTTCGACGAGAA 1111
DB  1053  GCACGACATAAGCGATGAGCCAGAGTGTAACAATACCTTTTCAACTTTGATTTTGAACCA 1112
QY  1112  GGCTTAAACGAGGACCAAAATGAAGCAGCTGATCTTCAACGAGGATCGAGATGAACCC 1171
DB  1113  TGCACTCTCAGAGGAGCAGATGAAGAACTAATCTACCGGAGGCGCTTGCTTTCAATCC 1172
QY  1172  AAACATCCGGTACTAG 1187
DB  1173  AGAATATCAGCAATAG 1188

RESULT 8
US-09-938-842A-644
; Sequence 644, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIP300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 644
; LENGTH: 1188
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-644

Query Match          36.4%; Score 508.8; DB 3; Length 1188;
Best Local Similarity 67.2%; Pred. No. 1.3e-137;
Matches 736; Conservative 0; Mismatches 357; Indels 3; Gaps 1;

QY  92  GGTGGCGGAGTTTCAGCGCGAGATGACGCGCGGATGACGCGCGGCTACCTCTACGACATCTT 151
DB  96  GATTGAGAAATATTCGCGCGACTCTTAGCCATGTTGGTGTATTTATTCAGTATAACATATT 155

QY  152  CGGGAACAAGTTTCGAGGTGACGAAACAAGTACCAAGCCGCCCATCATGCCCATTTGGCGCGG 211
DB  156  TGGAAACATCTTCGAGGTCAACCGCTAAGTATAAGCTCCGATCATGCTTATTTGGCAAGGG 215

QY  212  CGCTACGGGATCGTCTGCTCGTGATGAACTTTTGAGACGAGGAGATGTTGGCGGATAAA 271
DB  216  TGCTTATGGCATCGTTTGTTCGGCTATGAATCTGAAACTTAACGAGAGCGTTGCGATTAA 275

QY  272  GAAGATCGCAACGCTTCAACACGACATGAGCGCAAGCCAGCGCAGCTCGGGAGATCAA 331
DB  276  GAAATTTGCTAACGCTTTTGACAAATGAATGATGATTAAGAGGACTCTCCCGTGAGATCAA 335

QY  332  GCTCTCAGGACCTCGACCGGATGACGAAACATCATAGGCATCAGGGATGTGATCCCGCGCC 391
DB  336  GCTGCTTCGTCACATGATGATAAATATTTGTCATCAGAGATATTATCCCGCCACC 395

QY  392  GATCCCTCAGGCGTTCAACGAGCTCTACATTCGCCACGAGCTCATGGAACCGACCTCCA 451
DB  396  ATTAAGAAACGCTTTCAACGATGTTTACATTCGGTATGAGTTAAATGGACACTGATCTCCA 455

QY  452  TCACATCATCGCTCCAAACGAACTGTCCAGAGGACACTGCCAGTATTTCTGTACCA 511
DB  456  TCAATATCATTCGGTCAAAATCAAGCATTTACCGAAGAACATTTGCCAGTATTTCTTTACCA 515

QY  512  GATCTCTCGGGGCTCAAGTACATCCACTCGGCGAAGCTGATCCACCGGACCTGAAGCC 571
DB  516  GATCCCTCGGTGATTGAAATACATTCATCTGCAATATGCTTCACAGGAGTTTGAACC 575

QY  572  GAGCAACCTGCTGCTGAAACGCAACTTCGAGCTTCAAGATCTGCGACTTCGGGCTGGCGG 631
DB  576  AAGTAATCTCTCTCGAAGCGCAACTTCGCACTTAAATACTGCGATTTTGGGCTAGCTCG 635

QY  632  GCGTCTCGGAGAGGACATGATGACGGAGTACGTGTTCAACCGGTGGTACCGCGCGC 691
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QY  692  GGAGCTGCTGCTCAACTCCACCGACTACTCCGCGCGCATCGAGCTCTGGTCTCGGCTG 751
DB  696  AGAGCTTCTTTAAATCTTCTGATTAATCTGAGCTATCGATGTTTGGTCTGTAGGCTG 755

QY  752  CATCTTCAAGAGCTCATCAACCGCGAGCGCTCTTTCCCGGAGGAGGACACATGACCA 811
DB  756  TATTTTCATGGAGTTAATGAGCGTAAGCCACTCTTTCCCTGGACGAGATCATGTCCATCA 815

QY  812  GATGCGCTCATCACCGAGGTGATCGGGAGCGCGAGGACGAGCTGGGTTTCATAG 871
DB  816  GCTTCGCTTGTCTATGAGGCTCATAGGAATCTCCATCAGAGAAGAGCTCGAGTTCTT--- 872

QY  872  GAAACGAGGACCGGAGGAAGTACATGAGGCACTTCGCCGAGTACCCCGCGCGGACGTTCCG 931
DB  873  GAAACGAAACGCAAGGATACATAGACAGCTTCCACCTTATCTCTCGCAATCCATCAC 932

QY  932  GAGCATGTTCCCGCGGTTGAGCGCCCGCGCTTCGACCTCATCGAGAGAGTGTCACTTT 991
DB  933  TGAATAAGTTTCCCGACAGTGTCTTTTAGCTATAGACCTTATCGAGAAGATGTTAACT 992

QY  992  CAACCGCTGCAGAGATCACAGTTTCAGGAGGCGCTCGATCATCTTCTTACCTAGAGATT 1051
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QY 141 TACGACATCTTGGGAAACAGTTCCGAGTTCAGAACAGTACGACGCGCCCATCATGCC 200
Db |||||
QY 98 TACAACGTGTACGGGAACCTCTTCGAGGTCTCTTCAAGTACGCCCAACCCATCCGCCCC 157
Db |||||
QY 201 ATTGGCCGCGGCGCTTACGGGATCGTCTCTCGTGATGAACCTTTGAGACGAGGAGATG 260
Db |||||
QY 158 ATCGGTGCGGCGCTTACGGCATGTCTCGGGGTGTCACTCGCAGTCAGGGAGGAG 217
Db |||||
QY 261 GTGGCGATTAAGAGATGCCAACCGGTTCAACACGACATGACGCCAAGCGCAGCTC 320
Db |||||
QY 218 GTTGGATCAAGAGGTTGGCAATGCGTTGCAACACCATGACGCCAAGCGCAGCTC 277
Db |||||
QY 321 CGGAGATCAAGCTCTCAGGACCTCGACGAGAAATCATAGGCATCAGGAGATG 380
Db |||||
QY 278 AGGGAATCAAGCTGTGCGGCACATGGACCATGAGAACATCTTCCCTTAAAGGATGA 337
Db |||||
QY 381 ATCCCGCCCGCATCCCTCAGGCGTTCAACGAGCTTACATCGCCACGCGAGCTCATGGAC 440
Db |||||
QY 338 ATTGGCCGCCCACTAGAGAGAACTTTAATGAGTGTACATTGTTACTGAGTTAATGGAT 397
Db |||||
QY 441 ACGACCTCCATCACAATCATCCGCTCAACCGAAGAACTGTGAGAGAGCACTGCCAGTAT 500
Db |||||
QY 398 ACAGATCTCCATCAGATCGTAGCGCTCAAAATCAGCCATTGACTGATGATCATTTGCCAGTAC 457
Db |||||
QY 501 TTCTGTACAGATCTCGGGGGCTCAAGTACATCCACTCGCGAAGCTGTATCCACCGC 560
Db |||||
QY 458 TTCTGTATCAGTTGTACAGGGCTAAATAATGTGCACTCAGCAAAATATATTGCAACCGC 517
Db |||||
QY 561 GACCTGAAGCCGAGCAACCTGCTGTGAACGCCAACTGGGACCTCAAGATCTGCGACTTC 620
Db |||||
QY 518 GATCTGAGCCGAGCAATTTGTTCTTAATGCAATTTGACTCAAGATTGCAAGCTTT 577
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QY 621 GGCTGGCGGCGCGTGTGAGAGCGCAATGATCAAGAGTACGTGTGTCACCGCGTG 680
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QY 578 GGCTTTGCAAGGACCACTTCAGAGACAGATCTCATGACAGATGTGTGTCACTCGTTG 637
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QY 681 TACCGCGCGGAGCTGTCTCAACTCCAAGCTACTCCGCGCGCATCGAGTCTGG 740
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QY 638 TACCGGGCCACGAGCTGTGTGAACTGTTCACAGTACTCTGCTGCCATTGATGTCTGG 697
Db |||||
QY 741 TCCGTGCGGTGCATCTTATGAGCTCATCAACCGCGCGCGCTCTTCCCGCGAGGAC 800
Db |||||
QY 698 TCAATTGGATGATATAGTGAATGTTACTGTCGTAACCCCTGTTCTTGACGGGAT 757
Db |||||
QY 801 CACATGCCAGATGCGCTCATACCGAGGTGATCGGAGCGCCGACGAGACGAGCTG 860
Db |||||
QY 758 TACATCCAGCAATTAATAATGATCACTGAGCTCATAGGCTCTCCAGATGATGCAAGCTG 817
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QY 861 GGGTTTATAGGAACGAGGACGAGGAGTACATGAGGCACCTGCGCAGTACCGCGC 920
Db |||||
QY 818 GGATTTTTCGAAGTGATTAATGCAAAAGATATACAAACAACTACACAGTTTCCAAAG 877
Db |||||
QY 921 CGGACGTTTCGAGCATGTTCCCGGGTGCAGCGCGCGCTCGACCTCATCGAGAGG 980
Db |||||
QY 878 CAGGACTTCGCGCTGTTCCGCAATGTTCTTCCGCGCAGTCAATTTGTTGGAAGG 937
Db |||||
QY 981 ATGCTCACCTTCAACCGCTGACAGAAATCAGATTGAGAGCGCTCGATCATCTTAC 1040
Db |||||
QY 938 ATGCTTGTGTTGATCCAAGCAGCGGATTAACAGTTGATGAGGCTCTGCAATCATCATAC 997
Db |||||
QY 1041 CTAGAGAGATTGACGACATCGCGGATGAGCCCATCTGCTGAGGCGCTTCTCTTCGAC 1100
Db |||||
QY 998 TTGGCTTCACTTCATGAGATCAATGATGACCTTACCTGCGCTGCACCTTTTCACTTTGAT 1057
Db |||||
QY 1101 TTGAGCAGAGGCTCTTAAACGAGGACCAATCAAGCAGCTGATCTTCAACGAGGATC 1160
Db |||||
QY 1058 TTTGAGCAACCATCTTTTACAGAGCGCATATAAAGAACTCATCTGGAGGAACTTTTA 1117
Db |||||
QY 1161 GAGATGAACCAACATCCGGTACTAGATTGAA 1193
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QY 1118 GCATTTAAACGAGGCTCCCTACTAATCAAA 1150
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RESULT 12
US-10-425-115-86951/c
; Sequence 86951, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 86951
; LENGTH: 1803
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_179305C.1
US-10-425-115-86951

Query Match 34.8%; Score 485.8; DB 8; Length 1803;
Best Local Similarity 64.8%; Pred. No. 8.4e-131;
Matches 721; Conservative 0; Mismatches 392; Indels 0; Gaps 0;

QY 81 GACGGCGCGCGCTGCGGAGTTTCAGCGCGAGTTCAGCGCGAGTACGACGCGGCGCGGTACCTGCTC 140
Db |||||
QY 1524 GCGCGCGCGGTGGAGCGCAGATCAAGGGTATGGCGACGACGCGGGCGCTAGCTGCTG 1465
Db |||||
QY 141 TAGGACATCTTGGGAACAAAGTTTCAGGTGACGAACAGTACGACGCGCGCCATCATGCC 200
Db |||||
QY 1464 TACAACGTGTACGGAACCTCTTCGAGGTCTCTCCAAGTACGCGCCACCCATCCGCC 1405
Db |||||
QY 201 ATTGGCGCGCGCGCTTACGGGATGCTGCTCGGTGATGAACTTTGAGACGAGGAGATG 260
Db |||||
QY 1404 ATCGGTGCGCGCGCTTACGGCAATGTTCTCGCGGCTGTCTACTCGCAGTCAGGGAGGAG 1345
Db |||||
QY 261 GTGGCGATAAAGAAGATCGCCAAACCGGTTCAACAGCATGAGACGCCAAGCGCAGCTC 320
Db |||||
QY 1344 GTTGGATCAAGAGGTTGGCAATGCTTCGACCAACCAATCGACGCCAAGCGGACGCTC 1285
Db |||||
QY 321 CGGAGATCAAGCTCTCAGGCACTTCGACCAAGAGAACATCATAGGCAATCAGGAGTGTG 380
Db |||||
QY 1284 AGGGAATCAAGCTGCTGCGCCACATGGACCATGAGAACATCTTGGCTTTAAAGGATGA 1225
Db |||||
QY 381 ATCCCGCGCGCGATCCCTCAGGCGTTCAACGAGCTTACATCGCCACGAGCTCATGGAC 440
Db |||||
QY 1224 ATTGGCGCGCGCACTAGAGAGAACTTTAATGAGTGTACTTGTACTGAGTTAATGGAT 1165
Db |||||
QY 441 ACGGACCTCCATCACAATCATCCGCTCAACCAAGAACTGTGAGAGAGCACTGCCAGTAT 500
Db |||||
QY 1164 ACAGATCTCCATCAGATCGTAGCTCAATCAGCCATTGACTGATGATCATTTGCCAGTAC 1105
Db |||||
QY 501 TTCCTGTACAGATCTCGGGGGCTCAAGTACATCCACTCGCGGAACGTGATCCACCGC 560
Db |||||
QY 1104 TTTCTGTATCAGTTGCTACGAGGGCTAAATAATGTGCACTCAGCAAAATATATTGCAACCGC 1045
Db |||||
QY 561 GACCTGAAGCCGAGCAACCTGCTGTAACGCCCACTGCGACTCAAGATCTGCGACTTC 620
Db |||||
QY 1044 GATCTGAAGCCGAGCAATTTGTTCTTAAATGAAATTTGAGCTCAAGATTGAGACTTT 985
Db |||||
QY 621 GGCTGCGCGCGCGCTGCTGAGAGAGCGACATGATGACGAGTACGTGGTTCACCCGGTGG 680
Db |||||
QY 984 GGGCTTGAAGGACCACTTTCAGAGCAGATCTCATGACAGAGTATGTGGTCACTCGTTGG 925
Db |||||
QY 681 TACCGCGCGCGGAGCTGTCTCAACTCAACGACTACTCCGCGCGCATTCGACGCTG 740
Db |||||
QY 924 TACCGGCAACAGAGCTGCTGTTGAACCTTTCACAGTATCTGCTGCCATTCGATGCTG 865
Db |||||
QY 741 TCCGTGCGGTGCTCTTTCATGGAGCTCATCAACCGCGCGCGCTCTTCCCGCGAGGAC 800
Db |||||
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Db 864 TCAGTTGATGTCATAGTGGAATCGTTACTCGTCAACCCCTGTTTCTCGACGGAT 805  
QY 801 CACATCCACAGATCGCTCATCACGAGGTGATCGGACGCGCGACGACGAGCTG 860  
Db 804 TACATCCAGCAATTAATTAATGATCACTGAGCTCATAGGCTCTCCAGATGATGCAAGCCTG 745  
QY 861 GGGTTCCATACGAGACGAGGAGAGTACATGAGGACCTGCGGAGTACCGGCGC 920  
Db 744 GGATTTCTTGAAGTGATAATGCAAAAGATACATGAACAACCTACCAAGTTTCCAAGA 685  
QY 921 CGGACGTTCCGAGCATGTTCCGCGGTGCGAGCCGCGCGCTCGACCTCATCGAGAG 980  
Db 684 CAGGACTTCCGCTCGCTTCCGCAACATGTCTCTCGCGCAGTCGATTTGTTGGAAGG 625  
QY 981 ATGCTCACCTTCAACCCGCTGCAGAGAAACACAGTTTGAGAGGCGCTCGATCATCTTAC 1040  
Db 624 ATGCTTGTTGATCCAGCAGAGCGGATTAACGTTGATGAGGCTCTGCATCATCCATAC 565  
QY 1041 CTAGAGAGATTGACAGCATCGCGATGAGCCCATCTGCTCGAGCCCTTCTCTTCGAC 1100  
Db 564 TTGGCTTCACTTCATGAGATCAATGATGAACCTACCTGCCCTGCACCTTTTACGCTTTGAT 505  
QY 1101 TTCGAGCAGAGGCTCTAAACGAGGACCAATGAAGCAGCTGATCTTCAACGAGCGATC 1160  
Db 504 TTTGAGCAACCATCTTTACAGAAAGCGCATATAAAAGAACTCATCTGAGGGAATCTTTA 445  
QY 1161 GAGATGAACCCAAACATCGGTACTAGATTGAA 1193  
Db 444 GCATTTAACCCAGAGCTCCCTACTAATATCAA 412

RESULT 13  
US-10-437-963-36761/c  
; Sequence 36761, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 36761  
; LENGTH: 1717  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_40555C.1  
US-10-437-963-36761

Query Match 34.3%; Score 478.4; DB 7; Length 1717;  
Best Local Similarity 64.4%; Pred. No. 1.2e-128;  
Matches 716; Conservative 0; Mismatches 396; Indels 0; Gaps 0;  
QY 75 GGGATCGAGCGGCGCGGTGGCGGAGTTTCAGSCCGACGATGACGCGCGCGCGGTAC 134  
Db 1444 GCGCGCGGCGCGCGCGCGCGCGCGAGATCAAGGGGATGGGACGCGCGCGCGCGCTAC 1385  
QY 135 CTGCTCTACGACATCTTCGGGAACAAGTTGAGGTGACGAACAAGTACGAGCGCGCCATC 194  
Db 1384 GTGCTGTACAACGTGTACGGGAATCTTTCGAGGTCTCTCTCCAAGTACGCCCTCCCATC 1325  
QY 195 ATGCCCATTTGGCGCGCGCGCTACGGGATCGTCTCGTGTGATGAACTTTGAGGAGG 254  
Db 1324 CGCCCCATCGCGCGCGCGCGCTACCGGCATGTCTCGCGCGCTGTCTTAACCTCGGAGACGCG 1265

QY 255 GAGATGTTGGGATAAAGAGATGCCAAACGCTTCAAACAACGACATGGAACGCCAAGGCG 314  
Db 1264 GAGGAAGTTGGCAATCAAGAAGATTGGCAATGCATTCGACAACCATATCGATGCCAAGCGG 1205  
QY 315 AGCTTCCGGGAGATCAAGCTCTCAGGCACTTCGACCACTCGACCAAGCAATCATAGGCATCAGG 374  
Db 1204 ACATCTGAGAGAAATCAAGCTGTTCCGCCCATGAGGACCAAGCAATATATTTGCCATAAAG 1145  
QY 375 GATGTATCCCGCGCGCGATCCCTCAGCGGTTCAACGAGCTTACATCGCCACGCGAGCTC 434  
Db 1144 GACATAATTCGCCCGCCCAAGAGAGACAACTTTAATGATGTTTACATGTTTCTGAGTTG 1085  
QY 435 ATGAGACCGGACCTCATCATCATCATCGCTCCAAACCAAGAACTGTCAAGAAGACGACTGC 494  
Db 1084 ATGATATCTGATCTCCATCAGATCATACGCTCAATCAACCATTTGACTGATGACCACTGC 1025  
QY 495 CAGTATTTCTGTATACAGATCTCGGGGGCTCAAGTACATCCATCTCGCGCAACCTGATC 554  
Db 1024 CAGTACTTCTGTATACAGTGTCTACGAGGCTAAATATATGTCACTCGGCAAAATGTCTTG 965  
QY 555 CACCGGACCTGAAAGCGAGCAACCTGTCTGTGCTGACGCAACTGCGGCTCAAGATCTGC 614  
Db 964 CACCGTGTATGAAAGCAAGCAATTTGTCTTAAATGCAAAATTTGATCTCAAGATGCT 905  
QY 615 GACTTCGGGCTGGCGCGCGCTCGTCTGAGAGCGACATGATGACGAGTACGTTGCTCACC 674  
Db 904 GATTTGGGCTTGCAGAAACCACTACGAGACTGACCTCATGACAGAGTATGTGCTACT 845  
QY 675 CGGTGTTACCGCGCGCGAGCTGTCTCAACTCAACGACTACTCGCGCGCCATCGAC 734  
Db 844 CTTGTTATCGAGCACACAGAGCTGTCTGTGAATCTCTCGCAGTATCTGCTCTATTGAT 785  
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Db 784 GTCTGTTGAGTTGGATGCTACTTTGGTGAATTTGACTCGTCAACCCCTGTTTCTGGA 725  
QY 795 AGGACACATGACACAGATCGCTCATCACCGAGGTGATCGGACGCGCGACGCGAC 854  
Db 724 AGGGATTACATTCAGCAACTAAATTTGATCACTGAGCTGATAGGTTCCGCGAGTACTCA 665  
QY 855 GAGCTGGGGTTTCATACGGAACGAGGACGCGAGGAAAGTACATGAGGCACTTCCCGGAGTAC 914  
Db 664 AGCTTAGGTTTCTTCGGAGTGATAATGCAAGAAGATACATGAACAAGTACACAGTAC 605  
QY 915 CGCGCGCGAGCTTCCGCGAGCATGTTCCGCGGGTGCAGCGCGCGCTCGACCTCATC 974  
Db 604 CCAAGGCGAGGACTTCCGCTTCCGCAACATGTCTGTGTGTCAGTCTGTTTCTGTA 545  
QY 975 GAGAGATGCTCACCTTCAACCCGCTGCAGAGAATCACAGTTTGAGGAGGCGCTCGATCAT 1034  
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QY 1035 CTTTACCTAGAGAGATTGACGACATCCCGCATGAGCCCATCTGCTGAGGCGCTTCTCC 1094  
Db 484 CCATACTTGGCTTCTCTTCATGACATCAATGAAGAACCACCTCGCGCGAGCAGCTTTCAGC 425  
QY 1095 TTCGACTTCGAGCAGAGGCTCTAAACGAGGACCAATGAAGCAGCTGATCTTCAACGAA 1154  
Db 424 TTTGATTTGAGCAACCATCTTTTACTGAAGAACAATATAAAGAAGTCTATCTGGAGGAA 365  
QY 1155 GCGATCGAGATGAACCCAAACATCCGGTACTA 1186  
Db 364 TCTTGGCATTTAATCCGGATCTCTCCCTACTA 333

RESULT 14  
US-10-425-114-6328  
; Sequence 6328, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua



Qy	709	CCACCGACTACTCGCGCGCATCGACGTCTGGTCCGTGGCTGCTCATCTTTCATGAGCTCA	768
Db	1143	CCTCTGATTACACCTCTGCTATAGATGTGTGCTGTGTTGCATCTTTATGGAGCTTA	1202
Qy	769	TCACCGCCAGCGGCTCTCCCGCGAGGACCAATGACACAGATGCGCCTCATCACCG	828
Db	1203	TGAATAAAAGCCTCTGTTTCGGGCAAGACCATGTGATCAGATGCGCTTATTGACAG	1262
Qy	829	AGGTGATCGGAGCGCGACGACGAGCTGGGGTTTCATACGGAACGAGGACGCGAGGA	888
Db	1263	AGCTTCTTGGCACCCCAACTGAGGCTGACCTTGGGTTAGTGAATAATGAAGATGCAAGAA	1322
Qy	889	AGTACATGAGGCACTGCGCGAGTACCGCGCGGACGTTTCGCGAGCATGTTCCCGCGGG	948
Db	1323	GATATATCAGACAACTTCCTCAATATCCTCGCCCAACCTTTAGCTCAAGTCTTCCCCCATG	1382
Qy	949	TGCAGCCCGCGGCTCGACCTCATCGAGAGGATGCTCACTTCAACCGCTGCGAGAA	1008
Db	1383	TTCATCCGGCAGCCATTGATCTTGTGATAAAATGTTGACAGTTGATCCCCACCAAGAA	1442
Qy	1009	TCACAGTTGAGGAGGCGCTCGATCATCTTACCTAGAGAGATTGCAAGACATCGCCGATG	1068
Db	1443	TTACAGTTGAAGAGCACATAGCCCATCCATACCTTGAAAACTGCATGATGTAGCTGATG	1502
Qy	1069	AGCCCATCTGCTTGGAGCCCTTCTCCTTCGACTTCGAGCAGAAGGCTCTAAACGAGACC	1128
Db	1503	AACCAATCTGCATGGAGCCATTTTCATTTGATTTTGAGCAACAACAATTTGGATGAAGGC	1562
Qy	1129	AAATGAAGCAGCTGATCTTCACGAAGCGATCGAGATGAACCC	1171
Db	1563	AAATAAAGAGATGATCTACAGGGAAGCATTAGCACTCAATCC	1605

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Job time : 843 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 29, 2005, 05:17:30 ; Search time 195 Seconds  
(without alignments)  
3752.939 Million cell updates/sec

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Perfect score: 1396  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4172979 seqs, 262114271 residues  
Total number of hits satisfying chosen parameters: 8345958

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA New.\*  
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2: /cgn2\_6/prodata/2/pubpna/US06\_NEW\_PUB.seq.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	337.2	24.2	1866	US-10-955-054A-5	Sequence 5, Appli
2	278.8	20.0	1888	US-10-770-726-25	Sequence 25, Appl
3	258	18.5	1611	US-11-186-284-114	Sequence 114, App
4	234	16.8	2737	US-10-909-125-861	Sequence 861, App
5	161.4	11.6	2525	US-10-770-726-5	Sequence 5, Appli
6	141	10.1	2372	US-10-857-780-11	Sequence 11, Appl
7	135.4	9.7	3131	US-10-770-726-28	Sequence 28, Appl
8	128	9.2	983	US-10-770-726-9	Sequence 9, Appli
9	104.2	7.5	2328	US-10-770-726-7	Sequence 7, Appli
10	95.6	6.8	3073	US-11-113-424-11	Sequence 11, Appl
11	92	6.6	1400	US-10-750-185-28925	Sequence 28925, A
12	75.8	5.4	1474	US-10-770-726-8	Sequence 8, Appli
13	63.6	4.6	2838	US-10-770-726-27	Sequence 27, Appl
14	63	4.5	2497	US-10-750-185-35100	Sequence 35100, A
15	60.4	4.3	3527	US-10-770-726-35	Sequence 35, Appl
16	59.8	4.3	1254	US-10-966-483-32	Sequence 32, Appl
17	59.8	4.3	1254	US-11-021-441-16	Sequence 16, Appl
18	59.8	4.3	1392	US-11-000-365-49	Sequence 49, Appl
19	59.8	4.3	1437	US-11-032-794-49	Sequence 49, Appl
20	59.8	4.3	1437	US-10-966-483-35	Sequence 35, Appl
21	59.8	4.3	1437	US-11-021-441-19	Sequence 19, Appl
22	59.8	4.3	3105	US-10-966-483-19	Sequence 19, Appl
23	59.8	4.3	3105	US-11-021-441-3	Sequence 3, Appli

24	59.8	4.3	3963	6	US-10-966-483-1	Sequence 1, Appli
25	59.2	4.2	1636	6	US-10-981-029-6	Sequence 6, Appli
26	57.6	4.1	1639	6	US-10-770-726-21	Sequence 21, Appl
27	57.4	4.1	5221	6	US-10-821-234-367	Sequence 367, App
28	57.2	4.1	2030	7	US-11-111-239-1	Sequence 1, Appli
29	57	4.1	1371	6	US-10-451-375-5	Sequence 5, Appli
30	57	4.1	3832	6	US-10-821-234-99	Sequence 99, Appl
31	55.4	4.0	5745	6	US-10-750-185-54380	Sequence 54380, A
32	54.8	3.9	2545	7	US-11-099-691-15	Sequence 15, Appl
33	54.2	3.8	1142	6	US-10-451-375-1	Sequence 1, Appli
34	54.2	3.8	1065	6	US-10-750-185-58025	Sequence 58025, A
35	52.6	3.8	2310	7	US-11-073-579-1	Sequence 1, Appli
36	52	3.7	1593	6	US-10-858-730-138	Sequence 138, App
37	52	3.7	1680	6	US-10-770-726-37	Sequence 37, Appl
38	51.8	3.7	6058	6	US-10-770-726-17	Sequence 17, Appl
39	51.4	3.7	1278	6	US-10-750-185-52966	Sequence 52966, A
40	51.2	3.7	1427	7	US-10-770-726-11	Sequence 11, Appl
41	50.8	3.6	6890	7	US-11-005-029-1	Sequence 1, Appli
42	50.6	3.6	409	7	US-11-108-172-176	Sequence 176, App
43	49.6	3.6	3513	6	US-10-858-730-142	Sequence 142, App
44	49.2	3.5	2213	6	US-10-770-726-31	Sequence 31, Appl
45	49.2	3.5	35893	6	US-10-860-436-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-10-955-054A-5  
; Sequence 5, Application US/10955054A  
; Publication No. US20050266420A1  
; GENERAL INFORMATION:  
; APPLICANT: PUSZTAI, LAJOS  
; APPLICANT: SYMANS, W. FRASER  
; APPLICANT: HESS, KENNETH R.  
; APPLICANT: AVERS, MARK  
; APPLICANT: STEC, JAMES  
; TITLE OF INVENTION: MULTIGENE PREDICTORS OF RESPONSE TO CHEMOTHERAPY  
; FILE REFERENCE: UTXC:8800S  
; CURRENT APPLICATION NUMBER: US/10/955,054A  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 195  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 1866  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-955-054A-5

Query Match	24.2%	Score 337.2;	DB 6;	Length 1866;
Best Local Similarity	61.3%	Pred. No. 8.3e-68;		
Matches	603;	Conservative	0;	Mismatches 363;
				Indels 18;
				Gaps 3;
Qy	182	CCAGCGCCCATCATGCCATTCGGCGCGCGCTACGGGATCGTCTGCTCCGTGATGAA	241	
Db	195	CTACAGCGATTCGATACATCGCGAGGCGCGTACGGATGTCAGCTCGGCTATGA	254	
Qy	242	CTTTGAGACAGGAGATGGTGGCGATAAAGAGATCGCCACCGGTTCAACACGACAT	301	
Db	255	CCAGTGGCGAAGCTCGGTGGCCATCAAGAGAT--CAGCCCTTCGAACATCAGAC	311	
Qy	302	GGAGCCAGCGCACGCTCGGGAGATCAAGCTCTCAGGCACTCGACACAGAACAT	361	
Db	312	CTACTCCAGCGCACGCTCGGGAGATCCAGATCTCTGCTGCGCTTCGCGCATGATGT	371	
Qy	362	CATAGCCTCAGGATGTGATCCCGCGCGATCCCTCAGCGGTTCAACGCTCTACAT	421	
Db	372	CATCGGATCCGAGACATTCGCGGCGTCCACCTGGAGCCATGAGATGTCTACAT	431	
Qy	422	CGCCAGCGAGCTCATGGACACCGACCTCCATCATCATCATCCGCTCCAAACAGAACTGC	481	
Db	432	TGTGACGAGCCTGATGGAGACTGACCT---GTACAGTTGCTGTAAGCCAGCAGCTGAG	488	



482 AGAAGACACTGCCAGTATTTCCTGTACCAGATCTCTCGGGGGCTCAAGTACATCCACTC 541  
489 CAATGACCATATCTGTCTACTTCTCTTACCAGATCTCTCGGGGGCTCAAGTACATCCACTC 548  
542 GGGGAACGTGATCCACCGGACCTGAAGCGGAGCAACTGTCTGTCTGAAGCGCACTGCGA 601  
549 CGCAACGTGCTCCACCGGATCTAAAGCCCTTCAACCTGTCTCAGCAACACCACTGCGA 608  
602 CTTCAAGATCTGGAGCTTCGGGCTGGCGG-----CGTGTCTGGAGAGCGA 649  
609 CCTTAAGATTGTGATTTGGCTCTGGCCCGGATGTCGGATCTTGAGCATGACACACCGG 668  
650 CATGATGACGGATAGTGTGTCAACCGGTGTGTACCGCGCGCGGAGCTGTCTCAACTC 709  
669 CTTCTGTGACGGATGATGT 728  
710 CACCGACTACTCGCGCGCATGTGACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 769  
729 CAAAGGCTATACCAAGTCCATCGACATCTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 788  
770 CAAACCCAGCGCTCTTCCCGGAGGAGCACATGCACACAGATGGCTCTATCACCGA 829  
789 CTTCAACCGGCCCATCTTCTGT 848  
830 GTGTATCGGGAACCGGACGAGACGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 889  
849 CATCTCTGGCTCCCATCCAGGAGGACCTGAATTGTATCATCAACATGAAGGCCCGA 908  
890 GTACATGAGCCACTCTCGGAGTACCGCGCGCGGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 949  
909 CTACCTACAGTCTCTGCTTCCAGACCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 968  
950 GCAGCCCGCGCTCGACCTCATCGAGAGGATGTCTCACTCAACCGCTGCAGAGAT 1009  
969 AGACTCAAAGCCCTTGACTGT 1028  
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1029 CACAGTGGAGGAGCGCTGTCTCACCCCTACCTGGAGCAGTACTATGACCCGAGCATGA 1088  
1070 GCCCATCTGCTGGAGCCCTTCTCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 1129  
1089 GCCAGTGGCGAGGAGCCCTTCACTTTCGCTGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1148  
1130 AATGAAGCAGCTGATCTTCAACGA 1153  
1149 GCTGAAGGAGCTCATCTTCCAGGA 1172

RESULT 2  
US-10-770-726-25  
; Sequence 25, Application US/10770726  
; Publication No. US20050266409A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Brown, Eugene  
; APPLICANT: Liu, Wei  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING  
; FILE REFERENCE: AM101079 (031896-010000)  
; CURRENT APPLICATION NUMBER: US/10/770,726  
; CURRENT FILING DATE: 2004-02-04  
; NUMBER OF SEQ ID NOS: 48640  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 25  
; LENGTH: 1888  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-770-726-25

Query Match 20.0%; Score 278.8; DB 6; Length 1888;  
Best Local Similarity 56.5%; Pred. No. 1.7e-54;  
Matches 586; Conservative 0; Mismatches 437; Indels 15; Gaps 3;

QY 149 CTTGGGAACAAGTTTCGAGGTGAGAAACAAGTACACAGCGCCCATCATGTCCTTGGCGG 208  
DB 137 CGTCAACAGACCGCTCGGAGCTGCCAAGACCTACGTGTCCCAGACGACGTGGCAG 196  
QY 209 CGGCGCTTACCGGATTCGTCTCGTGTATGAACCTTTTGAAGACGAGGAGATGGTGGCGAT 268  
DB 197 CGGGCCCTATGGCTCGGTGTCTCGCCATCGACAAGCGGTGAGGGAGAGGTGGCCAT 256  
QY 269 AAGAGAGATCGCCAAACGGTTCAACAAGCATGGAACCGCAAGCGCATCGTCTCGGGAGAT 328  
DB 257 CAAGAAGCTGAGCGACCTTTTCAGTCCGAGATCTTTCGCAAGCGGCTACCGGAGCT 316  
QY 329 CAAAGCTCTCAGGCACTCGACCAAGAGAAATATAGGCATCAGGAGTGTGATCCCGCC 388  
DB 317 GCTGCTGTGAAGACATGAGCATGAGAAAGTCAATTGGGCTCTTGGATGTCTTCAACCC 376  
QY 389 GCGGATCTCTAG---GGTTCAACGACGTCTATCATCGCCACGAGCTCATGGAACCGA 445  
DB 377 AGCCTCTCTCCCTGCGCAACTTCTATGACTTCTACCTGGTGTGCTTCTCATGCAACGA 436  
QY 446 CTTCCATCACATCATCCGCTCCAAACCAAGACTGTCAAGAGACTGCCAGTATTTCT 505  
DB 437 TCTGAGAGATCATATGGG-----GATGAGTTCAGTGAGGAGAAAGTCCAGTACCTGT 490  
QY 506 GTACCAGATCTCGGGGGCTCAAGTACATCCACTCGGCGAACTGTATCCACCGGACCT 565  
DB 491 GTATCAGATGTCAAAGGCTTTAGTACATCCACTCTGCTGGGTCGTGCAACGAGGACCT 550  
QY 566 GAAGCCGAGCAACTGTGTGTGAACGCACTGTGCACTCAAGATCTCGGACTTCGGGT 625  
DB 551 GAAGCCAGGCAACTGTGTGTGAAGTGAAGACTGTGAAGTCTGAAGTCTTGGATTTGGGCT 610  
QY 626 GCGCGGCGCTGTGCGAGAGGACATGATGACGAGTACGTGTGTGACCGCGGTGATCCG 685  
DB 611 GCGCGGAC-----ATGCAAGCGCGAGATGATGTGTGTGTGTGTGTGTGTGTGTGTGT 664  
QY 686 GCGCGGAGCTGTGTCTCAACTCCACGACTTACTCCCGCCATCTGACGTCTGTGTCTGT 745  
DB 665 AGCCCCGAGGTGATCTTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 724  
QY 746 GCGGTGATCTTCAATGAGTGTATCAACCGCAGCGCTTCTTCCCGCAGGAGCAACAT 805  
DB 725 GSGGTGTATATGCGAGAGATGTGACAGGGAATACTCTGTTCAAGGGGAAAGATTACCT 784  
QY 806 GCACAGATGCGCTCATCAGGAGTGTGAGGAGCGGACGAGCAGGAGCTGGGTT 865  
DB 785 GGAACGCTGACCCAGATCTCTGAAGTGAACCGGGGTGCTTGCACGAGTTTGTGAGAA 844  
QY 866 CATACGGAACGAGGACGAGAGTACATGAGGCACCTGCGCGAGTACCCCGCGGAC 925  
DB 845 GCTGAACGACAAAGGGCCAAATCTTATCCAGTCTTGCACAGACCCCGAGNAGA 904  
QY 926 GTTCGAGAGCATGTTTCCCGGGGTGACCCCGCGCTCGACCTTCATCGAGAGGATGT 985  
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QY 986 CACCTTCAACCGCTGCGAGATACAGTGTGAGAGGCGGTGATCATCTTACCTAGA 1045  
DB 965 GAGCTAGACGTGGAACAAGCGCTGACCGCGCGAGGCGCTTCAACCTTCTTTGA 1024  
QY 1046 GAGATTGACAGCATCGCGGATGAGCCCATCTGCTGTGAGCGCTTCTCTTCACTTCA 1105  
DB 1025 ACCCTTCGGGACCTGTGAGGAGAGACGAGGCGCCAGCAGCGGTTGTGATTCCTTAG 1084  
QY 1106 GCAGAGGCTCTAAACGAGGACCAATGAAGCAGCTGTATCTTCAACGAGGATCGAGAT 1165  
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QY 1166 GNAACCAACATCCGTA 1183  
DB 1145 CAGCCCCATTTCCCGGAA 1162



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; LENGTH: 2737
; TYPE: DNA
; ORGANISM: H. sapiens
US-10-909-125-861

Query Match      16.8%; Score 234; DB 6; Length 2737;
Best Local Similarity 58.2%; Pred. No. 3.1e-44;
Matches 439; Conservative 0; Mismatches 300; Indels 15; Gaps 1;

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DB 350 CTACGCTGCTCTGGACCTGATGGAAGCGACCTGACAGATCATCATCTCTCACAGCC 409
QY 476 ACTGTGAGAGAGCACTGCGAGTATTTCTGTACCAAGATCTCTGCGGGGCTCAAGTACAT 535
DB 410 CCTCACACTGGAACACGCTGCTACTTCTCTGTACCAACTGCTGCGGGGCTGAAGTACAT 469
QY 536 CCACTCGGCGAGCTGATCCACCGACCTGAGCGGAGCGACCACTGCTGTAAGCCAA 595
DB 470 GCACCTGGGCTCAGGTCACTCACCGGTGACCTGAAGCCCTCCAACTTATTGGTGAATGAGAA 529
QY 596 CTCGACACCTCAAGATCTGCGACTTTCGGGCTGGCGCG-----GCCGTCGTC 640
DB 530 CTGTGAGCTCAAGATTGGTGACTTTGGTATGGCTCTGGGCTGTGCACTTCGCCCTCA 589
QY 641 GGAGAGCGACATGATGACGAGTACGTGTGTCACCCGGTGGTACCGCGCCGAGCTGCT 700
DB 590 ACATCATGTACTTTCATGACTGAGTATGTGGCCACGCGCTGGTACCGTGGCGGAGCTCAT 649
QY 701 GCTCAACTCCACCGACTACTCCGCGCGCATCGACGCTCTGGTGGTGGTGGTGGTCTTTCAT 760
DB 650 GCTCTCTTTGCGATGAGTATACACAGGCTATTGACCTCTGGTCTGTGGGCTGCACTTTGG 709
QY 761 GGAGCTCATCAACCGCCAGCGCTCTTCCCGCGAGCGACCACTGACACAGATGGCCT 820
DB 710 TGAGATGCTGGCCGCGCGCGAGCTCTTCCAGGCGCAAAACTATGTACACAGCTACAGCT 769
QY 821 CATCACCGAGGTGATCGGAGCGCCGACGAGCGAGCTGGGGTTTCATACGGAACGAGGA 880
DB 770 CATCATGATGGTGTGGGTACCCCATCACAGCGGTGATTCAGGCTGTGGGGCTGAGAG 829
QY 881 CGCGAGGAGTACATGAGCACTTCGCGCAGTACCCGCGCGGACGTTTCGCGAGCATGTT 940
DB 830 GGTGCGGGGCTATATCCAGAGCTTGCCCAACGCGCAGCTGTGCCCTGGGAGACAGTGA 889
QY 941 CCGCGGGGTGACGCGCGCGCTCGACCTCATCGAGAGGATGCTCACTTCAACCGCT 1000
DB 890 CCCAGGTGCGGACCGCGGCGCTATCATCTGTGGGTGCTGCTGGTTCGAGCCAG 949
QY 1001 GCAGAGATCACAGTTGAGAGCGCTCGATCATCTTACCTAGAGAGATTGCAGACAT 1060
DB 950 CGCTCGCATCTCAGCAGCTGCTGCCCTTCGCCACCTTTCTCGCCCAAGTACCATATCC 1009
QY 1061 CGCGATGAGCCCATCTGCTGAGCGCTTCTCTTCGATTCGAGCAGAGGCTCTAAA 1120
DB 1010 TGATGATGAGCCCTGACTGTGCCCGGCTTTGACTTTGCTTGTACCGGAAAGCCCTCAC 1069
QY 1121 CGAGGACCAATGAAGCAGCTGATCTTCAACGAA 1154
DB 1070 TCGGGAGCGCATTAAGAGGCCATTGTGGCTGAA 1103

RESULT 5
US-10-770-726-5
; Sequence 5, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM101079 (031896-010000)
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; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 2525
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-726-5

Query Match      11.6%; Score 161.4; DB 6; Length 2525;
Best Local Similarity 51.4%; Pred. No. 1.1e-27;
Matches 428; Conservative 0; Mismatches 396; Indels 9; Gaps 2;

QY 210 GGCGCTACGGGATCGTCTGCTCGTGATGAATTTTGAGACGAGGAGATGGTGGCGATA 269
DB 1450 GGCACCTATGAGTGGTCTACAGACAAAGACAAAGAAACAGATGAATAATTTGGCTCTA 1509
QY 270 AAGAAGATCGCCACGCGTTCAAACACACATGGACGCGCAAGCGCACGCTCCGGGAGATC 329
DB 1510 AAGCGGCTGAAGATGGAGAGGAGAGGGGCTTTCCGATCACGCTCGCTGAGGAGATC 1569
QY 330 AAGCTCTCAGGCACCTCGACACAGAGAACATCATAGGCATCAGGATGTGATCCCGCG 389
DB 1570 AACACCATCTCAAGGCCAGCATCCCAACATCTGTCACCGTTAGAGAGATTTGTGTGGC 1629
QY 390 CCGATCTCTCAGGCGCTTCAAGACGCTTACATCGCCACGCGAGCTCATGGACACCGACCTC 449
DB 1630 AGCAACATGGACAAGATCTACATCGTGATGAATATGTGGAGCAGCACCTCAAGAGCCTG 1689
QY 450 CATCATCATCTCCGCTCCAAACCAAGAACTGTGAGAAGAGCATGCGCAGTATTTCTGTAC 509
DB 1690 ATGGAGAGCAATG-----AAACAGCCCTTCTCGCCAGGGGAGGTGAAGACCTGTATGATC 1743
QY 510 CAGATCTCGCGGGGCTCAAGTACATCACTCGCGCAAGCTGATCCACGCGACCTGAAG 569
DB 1744 CAGCTGCTGCGTGGGGTGAACACCTGCACGACAACTGGATCCTGCACCGCTGATCTCAAG 1803
QY 570 CCGAGCAACCTGCTGCTGTAAGCCAACTGCGACCTCAAGATCTCGGACTTCGGGCTGGCG 629
DB 1804 AGTCCAACTGCTGCTGAGCCACCGCGCATCTCAAGTGGGTGACTTCGGGCTGGCG 1863
QY 630 CGGCGGTC---GTGGAGAGGACATGATGACGAGTACGAGTACGCGGCTCACCGGTGTACCGC 686
DB 1864 CGGGAGTACGGATCCCTCTGAAGGCTTACACCCGCGTCTGTGGTGAACCTGTGGTACCGC 1923
QY 687 GCGCGGAGCTGCTGCTCAACTCCACCGACTACTCCGCGCCATCGAGCTCTGTGTCGCTC 746
DB 1924 GCCCAGAGCTGCTGCTGTGGTCCAGGAATACTCAAGGCGCTGACATGTGTCAGTGTG 1983
QY 747 GGCTGCATCTTCATGAGCTCATCAACCGCCAGCGCTTTCGCCGCGAGGGACCAATG 806
DB 1984 GGTTCATCTTCGGGAGCTGTGACTCAGAAGCTCTGTTCGCCGGAAGTCAGAAATC 2043
QY 807 CACCAAGATGCGCTCATCACGAGGTGATCGGGAACGCGGACGAGCAGAGCTGGGGTTC 866
DB 2044 GATCAGATCAACAGGTGTTCAAGGATCTGGGGAACCTTAGTGAGAAAAATCTGGGCGCGC 2103
QY 867 ATACGGAACGAGGACGCGAGGAGTACATGAGGACCTGCGCAGTACCCGCGCGGAGC 926
DB 2104 TACAGCGAGCTCCAGCAGATCAAGAGATGACTTTCAGGAGCACCCCTTCAACAACTC 2163
QY 927 TTCGCGAGCATGTTCCCGCGGTGAGCGCGCTCGAGCTTCATCGAGAGGATGCTC 986
DB 2164 CGCAAGCGCTTCGGGGCTCTGCTCTCAGACCAAGGCTTCGACCTCATGAACAGTTCCTG 2223
QY 987 ACCTTCAACCCGCTCGAGAGATCAAGTTGAGGAGGCGCTCGATCATCTCTTA 1039
DB 2224 ACCTACTTCCCGGGAGGAGATCAGCGCTGAGGACGCGCTCAAGCATGAGTA 2276

RESULT 6
US-10-857-780-11
```

```
; Sequence 11, Application US/10857780
; Publication No. US20050272043A1
; GENERAL INFORMATION:
; APPLICANT: ROTH, RICHARD B.
; APPLICANT: BRAUN, ANDREAS
; APPLICANT: KAMMERER, STEFAN M.
; APPLICANT: NELSON, MATTHEW ROBERTS
; APPLICANT: RENELAND, RIKARD HENRY
; APPLICANT: ROYAL-WRIGHTSON, CAROLYN R.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
; FILE OF INVENTION: THEREOF
; TITLE OF INVENTION: THEREOF
; CURRENT APPLICATION NUMBER: US/10/857,780
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 10/723,681
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/490,234
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: 60/525,239
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 4962
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-857-780-11

Query Match      10.1%; Score 141; DB 6; Length 2372;
Best Local Similarity 52.7%; Pred. No. 4,8e-23;
Matches 406; Conservative 0; Mismatches 350; Indels 15; Gaps 4;

QY 176 CAAGTACAGCGCCCATCATGCCATTGCGCGCGCGCTACGGGATCTCTGCTCCGT 235
DB 176 CAAGTACAGCGCCCATCATGCCATTGCGCGCGCGCTACGGGATCTCTGCTCCGT 235
QY 406 CAAGCGCTACCAAGCTTAAAGCTATTGGCTCTGGGGCTCAGGGCATAGTTGTGCGC 465
DB 406 CAAGCGCTACCAAGCTTAAAGCTATTGGCTCTGGGGCTCAGGGCATAGTTGTGCGC 465
QY 236 GATGAACCTTTGACAGGAGATGGTGGCGATTAAGAGATGCCAACCGTTCAACAA 295
DB 236 GATGAACCTTTGACAGGAGATGGTGGCGATTAAGAGATGCCAACCGTTCAACAA 295
QY 466 GTATGATGCTGTCTTGACAGAAATGTGGCCNTTAAGAACTCAGCAGACCTTTTCAGAA 525
DB 466 GTATGATGCTGTCTTGACAGAAATGTGGCCNTTAAGAACTCAGCAGACCTTTTCAGAA 525
QY 296 CGACATGGACGCGCAAGCGCGCTCCGGGAGATCAAGCTCTCAGGCACTCCGACACGA 355
DB 296 CGACATGGACGCGCAAGCGCGCTCCGGGAGATCAAGCTCTCAGGCACTCCGACACGA 355
QY 526 CCAACACATGCCAAGAGAGCTACCGGAGCTGCTCTCATGAGTGTGTGAACCATAA 585
DB 526 CCAACACATGCCAAGAGAGCTACCGGAGCTGCTCTCATGAGTGTGTGAACCATAA 585
QY 356 GAACATCATAGGCATCAGGATGTGATCCCGCCCGCGATCCCTC---AGCGTTCAACGA 412
DB 356 GAACATCATAGGCATCAGGATGTGATCCCGCCCGCGATCCCTC---AGCGTTCAACGA 412
QY 586 AATCATTTAGTTTATTAAATGTCTTACACCCAGAAAAGCTGGAGGATTTCCAAGA 645
DB 586 AATCATTTAGTTTATTAAATGTCTTACACCCAGAAAAGCTGGAGGATTTCCAAGA 645
QY 413 CGTCTACATCGCCAGGAGCTATGGACACGACCTCCATCATCATCCGCTCCACCA 472
DB 413 CGTCTACATCGCCAGGAGCTATGGACACGACCTCCATCATCATCCGCTCCACCA 472
QY 646 TGTCTACTAGTAATGGAACGTATGGATGCCAATTTATGTCAAGTGATTC-----AGAT 699
DB 646 TGTCTACTAGTAATGGAACGTATGGATGCCAATTTATGTCAAGTGATTC-----AGAT 699
QY 473 AGAAGTCTCAGAGAGCACTGCCAGTATTTCTGTACAGATCTCTGGGGGCTCAAGTA 532
DB 473 AGAAGTCTCAGAGAGCACTGCCAGTATTTCTGTACAGATCTCTGGGGGCTCAAGTA 532
QY 700 GGAATTAGACATGAGCGAATGTCTTACCTGTCTGTACCAATGTGTGTGCAATAGCA 759
DB 700 GGAATTAGACATGAGCGAATGTCTTACCTGTCTGTACCAATGTGTGTGCAATAGCA 759
QY 533 CATCTACTCGGCGAAGCTGTATCCACCGGACCTGGAACCGGAGCAACCTGCTGTGAACGC 592
DB 533 CATCTACTCGGCGAAGCTGTATCCACCGGACCTGGAACCGGAGCAACCTGCTGTGAACGC 592
QY 760 CTTCCATTCTGCTGGAATTTATCAGGGATTTAAACCAAGTAATTTAGTCAAGTC 819
DB 760 CTTCCATTCTGCTGGAATTTATCAGGGATTTAAACCAAGTAATTTAGTCAAGTC 819
QY 593 CAATCTGGACCTCAAGATCTGCGACTTCGGGCTGGCGGCGCTGCTGGAGAGCGCAT 652
DB 593 CAATCTGGACCTCAAGATCTGCGACTTCGGGCTGGCGGCGCTGCTGGAGAGCGCAT 652
QY 820 TGAATTGCATTTGAAATCTTGGACTTTTGAATCTGGCCAGGACAGGCAACAAGCTTCAT 879
DB 820 TGAATTGCATTTGAAATCTTGGACTTTTGAATCTGGCCAGGACAGGCAACAAGCTTCAT 879
QY 653 GATGACGAGTACGTGTGTCAACCGGTGTATCCGGCGCGGAGCTGCTCAACTCCAC 712
DB 653 GATGACGAGTACGTGTGTCAACCGGTGTATCCGGCGCGGAGCTGCTCAACTCCAC 712
QY 880 GATGACTCCATATGTGTGTGACACATTTATACAGAGCCCTGAGTCACTCT---GGGAT 936
DB 880 GATGACTCCATATGTGTGTGACACATTTATACAGAGCCCTGAGTCACTCT---GGGAT 936
QY 713 CGACTACTCCGCGCCCATCGACGCTCTGCTCGGCTGCGATCTTTCATGGAGCTCATCAA 772
DB 713 CGACTACTCCGCGCCCATCGACGCTCTGCTCGGCTGCGATCTTTCATGGAGCTCATCAA 772
QY 937 GGGCTACAAGGAGAACCTGGATATATGCTGTGGGATGATTTATGGAGAAATGGTTTCG 996
DB 937 GGGCTACAAGGAGAACCTGGATATATGCTGTGGGATGATTTATGGAGAAATGGTTTCG 996
QY 773 CGCGCAGCGCTCTTCCCGCGCGGAGACCAATGACAGATGGCGGCTCTCATCCCGAGGT 832
DB 773 CGCGCAGCGCTCTTCCCGCGCGGAGACCAATGACAGATGGCGGCTCTCATCCCGAGGT 832
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DB 997 CCACAAATCTCTTTCCAGGAGGAGCTATATTGACAGTGAATAAGTAATTGAACA 1056
QY 833 GATCGGACGCGACGAGCGAGCGAGCTGGGGTTTCATACGGAACGAGAGCCGAGGAAGTA 892
DB 1057 ACTAGGAACACCATGTCAGAAATTCATGAAG---AAATTGCAACCCACAGTAAGAACTA 1113
QY 893 CATGAGGACCTCGCGCAGTACCGCGCGGAGGTTTCGGGAGCATCTTCCC 943
DB 1114 TGTGGAGATCGCGCCCAAGTATGCGGAGCTCACCTTTCCCAAACTCTTCCC 1164

RESULT 7
US-10-770-726-28
; Sequence 28, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE OF INVENTION: CANCERS
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 3131
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-770-726-28

Query Match      9.7%; Score 135.4; DB 6; Length 3131;
Best Local Similarity 50.9%; Pred. No. 9.9e-22;
Matches 437; Conservative 0; Mismatches 401; Indels 21; Gaps 4;

QY 202 TTGGCGCGCGCGCTACGGGATGCTGTCTGCTCCGTGATGAACCTTTGACAGGAGATGG 261
DB 202 TTGGCGCGCGCGCTACGGGATGCTGTCTGCTCCGTGATGAACCTTTGACAGGAGATGG 261
QY 908 TGGCGGAGGTACCTATGCGCCGCTCTACAAAGGCAAAAGCAAGCTCACAGACAACTTG 967
DB 908 TGGCGGAGGTACCTATGCGCCGCTCTACAAAGGCAAAAGCAAGCTCACAGACAACTTG 967
QY 262 TGGCGGATGAAGAGATGCGCAACGCTTCAACACGACATGGAGCGCCAGCGACGCTCC 321
DB 262 TGGCGGATGAAGAGATGCGCAACGCTTCAACACGACATGGAGCGCCAGCGACGCTCC 321
QY 968 TGGCACTCAAGAGAT---CAGACTGGAACATGAAGGGGGCACCTCTGCACCGCATCC 1024
DB 968 TGGCACTCAAGAGAT---CAGACTGGAACATGAAGGGGGCACCTCTGCACCGCATCC 1024
QY 322 GGGAGATCAAGCTCTCAGGACCTCGACCAACGAGAACTCATAGGCAATCAGGAGATGA 381
DB 322 GGGAGATCAAGCTCTCAGGACCTCGACCAACGAGAACTCATAGGCAATCAGGAGATGA 381
QY 1025 GGGAGTGTCTCTCAAGGACCTCAACACGCGCAACATCGTTACGCTACATGACATTA 1084
DB 1025 GGGAGTGTCTCTCAAGGACCTCAACACGCGCAACATCGTTACGCTACATGACATTA 1084
QY 382 TCCCGCGCGCGATCTCCTCAGGCGCTTCAACGAGCTTACATCGGCAACGAGGCTCATGGACA 441
DB 382 TCCCGCGCGCGATCTCCTCAGGCGCTTCAACGAGCTTACATCGGCAACGAGGCTCATGGACA 441
QY 1085 TCCACACGAGAGAGTCCCTCACCTTGTCTTTGAGTACCTTGGACAGGACCTGAAGCAGT 1144
DB 1085 TCCACACGAGAGAGTCCCTCACCTTGTCTTTGAGTACCTTGGACAGGACCTGAAGCAGT 1144
QY 442 CCGACCTCCATCATCATCATCCGCTCCAAACCAAGAACTGTGAGAGAGCACTGCCAGTATT 501
DB 442 CCGACCTCCATCATCATCATCCGCTCCAAACCAAGAACTGTGAGAGAGCACTGCCAGTATT 501
QY 1145 ACCTGGAATGCTGTGGGAACATCATCAAC-----ATGCAACATGTGAACATGT 1192
DB 1145 ACCTGGAATGCTGTGGGAACATCATCAAC-----ATGCAACATGTGAACATGT 1192
QY 502 TCCTGTACACAGATCTCTCGGGGGCTCAAAGTACATTCACCTCGGGGAACTGATCCACCGCG 561
DB 502 TCCTGTACACAGATCTCTCGGGGGCTCAAAGTACATTCACCTCGGGGAACTGATCCACCGCG 561
QY 1193 TCCTGTTCAGTGTCTCCGTGGCTTACTGCGCACCGGAGAGAGTGTCTACACCGAG 1252
DB 1193 TCCTGTTCAGTGTCTCCGTGGCTTACTGCGCACCGGAGAGAGTGTCTACACCGAG 1252
QY 562 ACCTGAAGCGAGAACCTGCTGCTGTAACGCCAACTCGCGACCTCAAGATCTGCGACCTTCG 621
DB 562 ACCTGAAGCGAGAACCTGCTGCTGTAACGCCAACTCGCGACCTCAAGATCTGCGACCTTCG 621
QY 1253 ACCTCAAGCCCCAGAACCTGCTCATCAACGAGAGGGGAGAGCTCAAGCTGGCTGCTTTG 1312
DB 1253 ACCTCAAGCCCCAGAACCTGCTCATCAACGAGAGGGGAGAGCTCAAGCTGGCTGCTTTG 1312
QY 622 GCGTGGCGCGGCC---GTGCTCGGAGAGCACATGATGACGAGAGTACGTGCTCAACCGGT 678
DB 622 GCGTGGCGCGGCC---GTGCTCGGAGAGCACATGATGACGAGAGTACGTGCTCAACCGGT 678
QY 1313 GCGTGGCGCGGAGCAAGTCAATCCCAACAAAGACATACTCAATGAGGTGGTGAACATGT 1372
DB 1313 GCGTGGCGCGGAGCAAGTCAATCCCAACAAAGACATACTCAATGAGGTGGTGAACATGT 1372
QY 679 GGTACCGCGCGCGGAGCTGCTGCTCAACTCCACCGACTACTCCCGCGCGCATTCAGCGTCT 738
DB 679 GGTACCGCGCGCGGAGCTGCTGCTCAACTCCACCGACTACTCCCGCGCGCATTCAGCGTCT 738
QY 1373 GGTACCGCGCGCGCTGCTGCTGGGTCCAGGAGTACTTCCACTCAGATTGACATGT 1432
DB 1373 GGTACCGCGCGCGCTGCTGCTGGGTCCAGGAGTACTTCCACTCAGATTGACATGT 1432
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QY 739 GGTCCGTGGCTGCATCTTTCATGAGCTCATTAACCGCCAGCGCGTCTTCCCGGAGGG 798
|||
Db 1433 GGGGTGGGCTGCATCTTTCATGAGTGGCCACAGGCGGTCCCTCTTTTCGGGCTCCA 1492
|||
QY 799 ACCACATGACACAGATGCGCTCATCACAGAGTGATCGGAGCGCCGACGAGCGAGC 858
|||
Db 1493 CGGTGAGGACACAGCTACACTTCTTCGTATCTTAGAACCCCACTGAGGAGACT 1552
|||
QY 859 TGGGGTTTATACAGAAACGAGGACGCGAGGAAGTACATGAGGCACCTCGCGCATACCCGC 918
|||
Db 1553 GGCCAGGCATCTGTCCAAGGAGGTTCAAG--ACATACAACTACCCCAAGTACCGAG 1609
|||
QY 919 GCCGAGAGTTCCGAGAGATGTTCCCGGGTGCAGCCCGCGGCTCGACCTCATCGAGA 978
|||
Db 1610 CCAGAGCCCTTTTGAAGCCACGACCCCGACTTGTATAGCGACGGGGCCGACCTCTCACCA 1669
|||
QY 979 GGATGCTCACTTCAACCCGCTGCAGAGAAATCACAGTTGAGGAGGCGCTCGATCATCTT 1038
|||
Db 1670 AGCTGTTGCAAGTTTGAAGGTGGAATCGGATCTCCGAGAGGATGCCATGAAACATCCAT 1729
|||
QY 1039 ACCTAGAGAGATTGCACGA 1057
|||
Db 1730 TCTTCTCAGTCTGGGGA 1748
|||

RESULT 8
US-10-770-726-9
; Sequence 9, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 983
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-726-9

Query Match 9.2%; Score 128; DB 6; Length 983;
Best Local Similarity 50.6%; Pred. No. 3.4e-20;
Matches 429; Conservative 0; Mismatches 395; Indels 24; Gaps 4;

QY 201 ATTGGCCGGCGCGCTACGGGATCGTCTCGTGATGAACCTTTGAGACGAGGGAGATG 260
|||
Db 52 ATTGGGGAAGGCACCTACGGAACTGTGTTCAAGGCCAAAACCGGAGACTCATGAGATC 111
|||
QY 261 GTGGCGATTAAGAAGATTCGCCAACGGGTTCAACACGACATGAGACGCCAAGCGCAGCTC 320
|||
Db 112 GTGGCTCTGAACGGGTGAGGCTGGATGACGATGAGGGTGTGCGGAGTTCCGCCCTC 171
|||
QY 321 CGGGAGATCAAGCTCTCAGGCACCTCGACCCAGGAACATCATAGGCATCAGGAGTNG 380
|||
Db 172 CGGGAGATCGCCTACTCAAGGAGCTGAAGCAACAGAACATCGTCAGGCTTCATGACGTC 231
|||
QY 381 ATCCCGCCGCGCATCCCTCAGGCGTTCAACGAGCTCTACATCGCCAGGAGCTCATGGAC 440
|||
Db 232 CTGCACAGCGACAAGAAGCTGACTTTGGTTTTTGAATTTCTGTGACCAAGGACCTGAGAAG 291
|||
QY 441 ACCGACCTCCATCACAATCATCTCGCTCCAAACCAAGAACTGTTCAGAGAGCACTGCCAGTAT 500
|||
Db 292 T-----ATTTTGACAGTTGCAATGGTGACCTCGATCCTGAGATTGTAAAGTCA 339
|||
QY 501 TTCTCTTACAGATCTCGGGGGCTCAAGTATACCATCCACTCGGCGAAGCTGATCCACCGC 560
|||
Db 340 TTCTCTTCCAGCTACTAAAGGGCTGGGATTTCTGTATAGCGGCAATGTGTACTACAGG 399
|||
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```
QY 561 GACCTGAAGCCGAGCAACTGCTGCTGAAGCGCAACTGCGAATCTCAAGATCTGCGACTTC 620
|||
Db 400 GACCTGAAGCCCGAGAACTGCTTAATAAACAGAAATGGGAGCTGAAATTTGGCTGATTTT 459
|||
QY 621 GGGCTGGCGCGCGCTCGTCCGAGAGCGACATGA---TGACGAGTACGTGGTCAACCCGG 677
|||
Db 460 GGCCTGGCTCGAGCCCTTTGGGATTCCTCCGCTGTTACTCAGCTGAGGTGGTCACTG 519
|||
QY 678 TGGTACCGCGCGCGCGAGCTGCTGCTCAACTCCACCGACTACTCCGCGGCCACTCGACGTC 737
|||
Db 520 TGGTACCGCGCCACCGGATGTCTCTTTGGGGCCAAGCTGTACTCAGCTCCATCGACATG 579
|||
QY 738 TGGTCCGTGGCTGCATCTTCATGAGCTCATAAACC---GCCAGCCGCTCTTCCCGGC 794
|||
Db 580 TGGTCAGCGCGCTGATCTTTGCAAGCTGGCAATGCTGGGCGGCTCTTTTCCCGGC 639
|||
QY 795 AGGAGACCATGCAACAGATGGCCCTCATCACCAGGTGATCGGAGCGCGCGAGCGAC 854
|||
Db 640 AATGATGTCGATGACCGCTTGAAGAGGATCTTCCGACTGCTGGGACGCGCCACCGAGG 699
|||
QY 855 GAGCTGGGGTTTCATACCGAAACGAGGACGCGAGGAAGTACATGAGGCACCTGCGCGAGTAC 914
|||
Db 700 CAGTGGCCCTCTATGACCAAGCTGCCAG-----ACTATAAGCCCTATCCGATGTACCCG 753
|||
QY 915 CCGCGCCGAGCGTTCCGAGCATGTTCCGCGGGGTGCGAGCCCGCGCTCGACCTCATC 974
|||
Db 754 GCCACAACATCCCTGGTGAACTGCTGCGCCAAACTCAATGCCACAGGAGGATCTGCTG 813
|||
QY 975 GAGAGATGCTCACCTTCAACCCGCTGCAGAGAAATCACAGTTGAGAGGCGCTCGATCAT 1034
|||
Db 814 CAGAACTTCTGAAGTGTAAACCTCTCCAGCGTATCTCAGCAGAAAGAGGCCCTCGCAGCAC 873
|||
QY 1035 CCTTACCT 1042
|||
Db 874 CCTTACTT 881
|||

RESULT 9
US-10-770-726-7
; Sequence 7, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 2328
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-726-7

Query Match 7.5%; Score 104.2; DB 6; Length 2328;
Best Local Similarity 48.6%; Pred. No. 1.2e-14;
Matches 413; Conservative 0; Mismatches 418; Indels 18; Gaps 4;

QY 201 ATTGGCCGGCGCGCTACGGGATCGTCTCGTGATGAACCTTTGAGACGAGGAGATG 260
|||
Db 261 ATCGAGAGGCGCACTACGGAGTTGTATCAAGCCAGAAAACAGTTGACGGAGAGGTG 320
|||
QY 261 GTGGCGATAAAGAAGATCGCCAAACCGTTTCAACACGACATGAGACGCCAAGCGCAGCTC 320
|||
Db 321 GTGGCGCTTAAGAAAATCGCTCGACACTGAGAGTGGAGGGTGTGCCAGTACTGCCATC 380
|||
QY 321 CGGGAGATCAAGCTCTCAGGCACCTCGACCCAGGAACATCATAGGCATCAGGAGTNG 380
|||
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381 CGAGAGATCTCTGCTTAAAGAGCTTAACCATCTTAATATTTCTCAAGCTGCTGGATGTC 440  
381 ATCCCGCGCGGATCCCTCAGGCGTTCAACAGAGTCTATACGCGCCACGAGGCTCATGGAC 440  
441 ATTACACAGAAATAAATCTCTACCTGGTTTTTGAATTTCTGCACCAAGATCTCAAGAAA 500  
441 ACCGACTCCATCACATATCCGCTCAACCAAGACTGTCTCAGAGAGCACTGCCAGTAT 500  
501 -----TTCATGGATGCTCTCTCAC--TGGAATTCCTTCCCTTCATCAAGAGC 551  
501 TTCTCTACAGATCTCTGGGGGCTCAAGTATATCATCTCGCGGAACGTGATCCACCGC 560  
552 TATCTGTTCCAGTCTCTCAGGCGCTAGCTTTCTGCCATTTCTCATCGGCTCTCCACCGA 611  
561 GACCTGAAGCGAGCAACTCTGCTGTAAGCGCAACTGCGACCTCAAGATCTCGGACTTC 620  
612 GACCTTAAACCTCAGAATCTGCTTATTAACACAGAGGGGCGCATCAAGCTAGCAGACTTT 671  
621 GGGCTGGCGGGCGCTCTCGAGAGCGGACATGA---TGACGGAGTACGTGGTCAACCGG 677  
672 GGACTAGCCAGAGCTTTTGGAGTCCCTGTTCTGTACTTTACACCCATGAGGTGGTGAACCTG 731  
678 TGCTACCGCGCGCGAGCTGCTGCTCAACTCCACCGACTACTCCGCGCCATCGACGTC 737  
732 TGCTACCGAGCTCTGAAATCTCTCTGGGCTGCAATATTTTCCACAGCTGTGGACATC 791  
738 TGCTCGCTCGGCTGCTATCTTCTATGAGCTCATCAACCGCGAGCGCTCTTTCGCCGAGG 797  
792 TGAGCTCGGCTGCTATCTTTGCTGAGATGCTGACTCGCGGGCCCTATTTCCTCGGAGAT 851  
798 GACCACATGACAGATGCGCTCTACCGAGTGTATCGGAGCGCGGAGCGGAGGAG 857  
852 TCTGAGATTTGACAGCTCTTCGGGATCTTTTCGGACTCTTGGGGACCCCA-----GATGAG 905  
858 CTGGGTTTCATCGGAAGAGGAGCGGAGGAACTATCATGAGGCACTTCGCGCAGTACCCG 917  
906 GTGGTGTGGCAGAGTACTTCTATGCTGATTAAGCAAGTTTCCCAAGTGGGCC 965  
918 CGCGGAGCTTCGCGAGCATGTTCCCGGGGTGAGCGCGCGCTCGACCTCATCGAG 977  
966 CGGCAAGATTTTAAAGTTGTACTCCCTCGATGAGATGAGCGAGGCTGTTTATCG 1025  
978 AGATGCTACCTTCAACCGCTGACAGAGATCAGATTGAGAGGGCTGATCATCT 1037  
1026 CAAATGCTGACTACGACCCCTAAACGCGATTTTCGGCCAAAGCAGCGCTGGCTCACCT 1085  
1038 TACTAGAG 1046  
1086 TTCTTCAG 1094

RESULT 10

US-11-113-424-11  
; Sequence 11, Application US/11113424  
; Publication No. US20050260713A1  
; GENERAL INFORMATION:  
; APPLICANT: Gangolli et al.  
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-225  
; CURRENT APPLICATION NUMBER: US/11/113,424  
; CURRENT FILING DATE: 2005-04-21  
; PRIOR APPLICATION NUMBER: 60/256,704  
; PRIOR FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: 60/311,590  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/257,314  
; PRIOR FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: 60/311,613  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/315,617  
; PRIOR FILING DATE: 2001-08-29  
; PRIOR APPLICATION NUMBER: 60/307,506  
; PRIOR FILING DATE: 2001-07-24

; PRIOR APPLICATION NUMBER: 60/322,358  
; PRIOR FILING DATE: 2001-09-14  
; PRIOR APPLICATION NUMBER: 60/294,075  
; PRIOR FILING DATE: 2001-05-29  
; PRIOR APPLICATION NUMBER: 60/288,153  
; PRIOR FILING DATE: 2001-05-02  
; NUMBER OF SEQ ID NOS: 190  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 3073  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-113-424-11

Query Match

Best Local Similarity 6.8%; Score 95.6; DB 7; Length 3073;  
Matches 288; Conservative 0; Mismatches 299; Indels 3; Gaps 1;

QY 200 CATTGGCCGCGCGCTACGGGATGCTGCTGCTCGGTGATGAACCTTTGAGACGAGGAGAT 259  
DB 695 CATTGGCCGCGCGGCTTTGGCGAGTCTATGGGTCCCGAAGCTGACACAGCAGAT 754  
QY 260 GGTGGCGATAAAGAGATCGCCAAACGCGTTCAACACAGCATGAGCCCAAGCGCAGCT 319  
DB 755 GTACGCCATGAAGTGCCTGACAAAGAGCGCATCAAGATGAAGACAGGGGAGACCTGGC 814  
QY 320 CGGAGGATCAAGCTCTCAGGCACTCGACCACTCGACCAAGAGAAATCATAGGATCAGGATGT 379  
DB 815 CTTGAACGAGCGCATCATGCTCTCGCTCGTCAAGCTGCGGAGTCTGCTTCTGCTG 874  
QY 380 GATCCGCGCGCGGATCCCTCAGGCGTTCAACGAGCTCTACATCGCCACGAGGCTCATGA 439  
DB 875 CATGTATACGCGGTTCCACACGCGCAAGCTCAGCTTCATCTCTGACCTCATGAACCG 934  
QY 440 CACCGACTCCCATCATCATCATCGCTCCAAACCAAGAACTGTTCAGAAAGAGCACTGCCAGTA 499  
DB 935 TGGGAGCTTGCACTACCACTCTCCAGCAGCGGGTCTTCTCAGAGGCTGACATGCGCTT 994  
QY 500 TTTCTGTATACAGATCCTCGGGGGCTCAAGTATACCTCACTCGGCGAACTGATCCACCG 559  
DB 995 CTATGCGCGCGAGATCATCTCGGGCTTGGAGCAGATGCAACCCGCTTCGTGGTCTACCG 1054  
QY 560 CGACCTGAAGCGAGCAACTCTGCTGCTGAACCGCAACTCGGACCTCAAGATCTCGGACTT 619  
DB 1055 GGACCTGAAGCGCAGCAATCTCTTGGACGAGCATGCGCACGCGGATCTCGGACCT 1114  
QY 620 CGGGCTGGCGCGCGCTCGTGGAGAGCGACATGATGACGAGTAGTGTGCTCACCCTGGT 679  
DB 1115 GGGCTGGCTGTGACTTCTCCAGA---AGAGCCCCATGCCAGGCTGGGACCCACCG 1171  
QY 680 GTACCGCGCGCGGAGCTGCTCTCAACTCCACCGACTACTCCGCGCCCATCGAAGTGTG 739  
DB 1172 GTACATGGCTCGGAGGCTCTCGAAGAGGCGTGGGCTAGCAGACAGTGTCCGACTGTT 1231  
QY 740 GTCCGTGCGTGCATCTTTCATGAGCTCATCAACCGCAGCGCTCTTCC 789  
DB 1232 CTCTCTGGGTGCATGCTCTTCAAGTTGTGCGGGGGCACAGCCCTTCC 1281

RESULT 11

US-10-750-185-28925/c  
; Sequence 28925, Application US/10750185  
; Publication No. US20050260603A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: Denise, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-2



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; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28925
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Bovine 19866881174740
US-10-750-185-28925

Query Match      6.6%; Score 92; DB 6; Length 1400;
Best Local Similarity 56.9%; Pred. No. 6.2e-12;
Matches 189; Conservative 0; Mismatches 140; Indels 3; Gaps 1;

Qy 496 AGTATTCTCTGTACCAAGATCTCGGGGGCTCAAGTACATCCACTCGCGAAGTGATCC 555
Db 730 AGAGCTACTTGTTCAGCTGCTCCAGGGCTCTACTTTCTGCCACTCTCATTTGGGTCTGC 671

Qy 556 ACCGCGACCTGAAGCCGAGCAACCTGCTGCTGAACGCCAACTGCGACCTCAAGATCTGCG 615
Db 670 ACCGAGACCTCAAACTCTGATCTGTTATCAACGCAGATGGTCCATCAAGCTAGCAG 611

Qy 616 ACTTCGGCTGGCGCGCGCTGCTCGAGAGCG---ACATGATGACGGAGTAGTGCTCA 672
Db 610 ACTTCGGACTAGCCAGAGCTTTTGGGGTCCCTTTCATCTATTATACCGACGAGTGGTGA 551

Qy 673 CCGGGTGTGTACCGCGCGGAGCTGCTGCTCAACTCCACCGACTACTCGCGGCATCG 732
Db 550 CTCGTGGTACTGAGCACTGGAATCCTTCGGGCTGCAAACTACTCTCATAGCTGTGG 491

Qy 733 ACCTCTGGTCCGTCGGTGTGATCTTCATGAGCTCATCAACCGCCAGCGCTCTTCCCG 792
Db 490 ACATCTGGAGCTCGGTGCTATCTTTGCTGAGATGCTGACCACTGGGCCCTATTCTCG 431

Qy 793 GCAGGACCACTGCAACCGATCGGCTCATC 824
Db 430 GAGACTCTGAGATCAACCAACTCTTCCAGATC 399

RESULT 12
US-10-770-726-8
; Sequence 8, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 1474
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-726-8

Query Match      5.4%; Score 75.8; DB 6; Length 1474;
Best Local Similarity 51.4%; Pred. No. 3.1e-08;
Matches 201; Conservative 0; Mismatches 187; Indels 3; Gaps 1;

Qy 466 CCAACCAAGACTGTGAGAGAGCACTGCCAGTATTTCTGTACCAAGATCCTGCGGGGC 525
Db 550 CCCACCAAGCTTGCAGCGGAAACGATCAAGATCTGATGCGCAAGTTTCTAAGAGGCG 609

Qy 526 TCAAGTACATCCACTCGGGAAGCTGATCCACCGCACTGAGCCGAGCACTGCTGCG 585
Db 610 TAGATTCTTTCATGCAATTGCTTACCAGATCTGAGCCAGAGAACTTCTGG 669
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Qy 586 TGAACGCCAACTGCGACCTCAAGATCTCGGACTTCGGGCTGCGCGCGCTCGTCGGAGA 645
Db 670 TGAACAAGTGGTGAACAGAGTCAAGCTGGCTGACTTTTGGCTGCGCAGAACTTACAGTACC 729

Qy 646 GCGACATGATGACGGAGTACGTGGTCAACCCGGTGTGTACCGCGCGCGGAGCTGCTGCTCA 705
Db 730 AGATGGCACTTACACCCCGTGGTTGTACACTCTGTGTACCGAGCTCCCGAAGTTCTTCTGC 789

Qy 706 ACTCCACCGACTACTCTCCGCGCATCGAGCTGTGGTCCGTGCTGCTGCTGCTATCTTCATGGAGC 765
Db 790 AGTCCAC---ATATGCAACACCTGTGACATGTGGAGTGTGGCTGTATCTTTGCGAGAGA 846

Qy 766 TCATCAACCGCCAGCGCTCTTCCCGCGCAGGACACATGCACAGATGCGCCTCATCA 825
Db 847 TGTTCGTCGAAAGCTCTCTTCTGTGAAACTCTGAAAGCCGACCAAGTTGGGCAAAATCT 906

Qy 826 CCGAGGTGATCGGAGCGCGGACGAGCAGCA 856
Db 907 TTGACCTGATTGGGCTGCTCCAGAGGATGA 937

RESULT 13
US-10-770-726-27
; Sequence 27, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 2838
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-726-27

Query Match      4.6%; Score 63.6; DB 6; Length 2838;
Best Local Similarity 47.7%; Pred. No. 2.3e-05;
Matches 186; Conservative 0; Mismatches 204; Indels 0; Gaps 0;

Qy 399 CAGGCGTTCAACGACGCTCTACATCCCGACGGAGCTCATGGACACCGACTCTCATCATC 458
Db 1366 CTGGTGGGGGACGAGCTCTGGGTGGTCTATGGAGTTTCTTGAAGAGGCGCCCTCACCGAC 1425

Qy 459 ATCCGCTCCAAACCAAGAACTGTCAAGAGACACTGCCAGTATTTCTGTACCAGATCCCTG 518
Db 1426 ATCGTCAACCAACCAAGGATGAACGAGGAGCAGATCGCGCCGTGTGCTTCAGTGTCTG 1485

Qy 519 CGGGGGCTCAAGTACATCCACTCGCGCGAAACGATGATCCACCGCGACTCTGAAGCCGAGCAAC 578
Db 1486 CAGGCGCTGTGGTCTCCAGCCCGCGGCGTCTATCCACCGGACATCAAGAGCGACTCG 1545

Qy 579 CTGCTGTGAAAGCCCAACTGCGACCTCAAGATCTCGGACTTCGGGCTGCGCGCGCGCGCTCG 638
Db 1546 ATCTGCTGACCCATGATGGCAGGGTGAAGCTGTGAGACTTTTGGGTCTGCGCCCGAGGTG 1605

Qy 639 TCGGAGAGCGACATGATGACGAGTACGTGGTGCACCGGTGTACCGCGCGCGGAGCTG 698
Db 1606 AGCAAGGAAGTCCCGGAGGAAGTGGTGTGGGACGCCCTATGATGATGCCCCAGAG 1665

Qy 699 CTGCTCAATCCACCGACTACTTCGCGCGCACTCGAGCTGTGTCGCTCGGCTGCAATCTTC 758
Db 1666 CTCATCTCCCGCTTCCCTTACGGGCGAGAGGTAGACATCTGCTGCTGGGATATGTTG 1725

Qy 759 ATGGAGCTCATCAACCGCGAGCCGCTCTTC 788
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Db 1726 ATTGAGATGGTGGACGGAGGCCCCCTAC 1755

RESULT 14

US-10-750-185-35100  
; Sequence 35100, Application US/10750185  
; Publication No. US20050260603A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-2  
; CURRENT APPLICATION NUMBER: US/10/750,185  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 35100  
; LENGTH: 2497  
; TYPE: DNA  
; ORGANISM: Bovine 19866881358776  
US-10-750-185-35100

Query Match 4.5%; Score 63; DB 6; Length 2497;

Best Local Similarity 65.0%; Pred. No. 3e-05;  
Matches 93; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 561 GACCTGAAGCCGAGCAACCTGCTGCTGAACGCCAACTGGACCTCAAGATCTGCGACTTC 620  
Db 1338 GATCTGAGCCTAGTAACATTTAGTAAAGTCAGACTGCACCTGAAGATCTCTCGACTTT 1397  
QY 621 GGCTGGCGGGCCGCTGCTGGAGAGGACATGATGACGGAGTACGTGTCAACCCGGTGG 680  
Db 1398 GGCTGGCTGCTACAGCGTGCCAACTTTATGATGACTCCCTATGTGTGTCACACGGTAT 1457  
QY 681 TACCGGCGCGGAGCTGCTGCT 703  
Db 1458 TACCGGCGACCTGAAGTCATCCT 1480

RESULT 15

US-10-770-726-35  
; Sequence 35, Application US/10770726  
; Publication No. US20050286409A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Brown, Eugene  
; APPLICANT: Liu, Wei  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING  
; FILE REFERENCE: AM101079 (031896-010000)  
; CURRENT APPLICATION NUMBER: US/10/770,726  
; CURRENT FILING DATE: 2004-02-04  
; NUMBER OF SEQ ID NOS: 48640  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 35  
; LENGTH: 3527  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-770-726-35

Query Match 4.3%; Score 60.4; DB 6; Length 3527;

Best Local Similarity 46.9%; Pred. No. 0.00013;  
Matches 227; Conservative 0; Mismatches 251; Indels 6; Gaps 1;

QY 292 ACAACGACATGGAGCGCAAGCGACGCTCCGGGAGATCAAGCTCTCAGGACACTCGACC 351

Db 1484 ACAACCTCTCTGCACCAGCAGATGCTGCAGTCGGAGATCCAGGCCATGAAGAAGTCGGCG 1543  
QY 352 ACGAGAACATCATAGGCAATCAGGATGTGATCCCGCGCCGATCCCTCAGGGGTTCAACG 411  
Db 1544 ACAAAACACATCTCGGCGCTGTACGCCGTGTCTCGTGGGGGACCCCGTGTACATCATCA 1603  
QY 412 ACGTCTACATCGCCACGGAGCTCATGGACACCGACCTCCATCACATCATCCGCTCCAAC 471  
Db 1604 CCGAGCTCATGGCCAAAGGGGACCTCTGGAGACTGCTCG-----CGACTCTGATGAGA 1657  
QY 472 AAGAACTGTGAGAAGAGCACTGCCAGTATTTCTGTACAGATCTCTGCGGGGCTCAAGT 531  
Db 1658 AAGTCTGCGCGTTTTCGGAGCTGTGGACATCGCTGGCAGGTGGCTGAGGGCATGTGT 1717  
QY 532 ACATCCACTCGCGGAACGTGATCCACCGGACCTGAAGCCGAGCAACCTGCTGCTGAACG 591  
Db 1718 ACCTGGAGTGCAGAAATTAATCCACCGGGACCTGGCCGCCAGGAACATCTCTGTCGGG 1777  
QY 592 CCAACTGGGACCTCAAGATCTCGGACTTGGGCTGGCGGCGCTGCTCGGAGAGCGACA 651  
Db 1778 AAAACACCTCTGCAAGTTGGGGACTTCGGGTAGCCAGGCTTATCAAGGAGGAGCTCT 1837  
QY 652 TGATGACGGAGTACGTGTGTCAACCGGTGTACCGCGCGCGGAGCTGTGCTCAACTCCA 711  
Db 1838 ACCTCTCCATGACCCACATATCCCTTACAAGTGGAGCGGCCCTGAAGCGCTCTCCGAG 1897  
QY 712 CCGACTACTCCCGCGCATCGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 771  
Db 1898 GCCATTACTCCACCAAAATCCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1957  
QY 772 ACCG 775  
Db 1958 GCAG 1961

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Job time : 198 secs

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OM protein - protein search, using sw model

Run on: December 27, 2005, 20:36:37 ; Search time 13 Seconds  
(without alignments)  
201.913 Million cell updates/sec

Title: US-10-768-886-2  
Perfect score: 1953  
Sequence: 1 MDGAPVAEPRPTWTHGGRYL.....DQMKQLIFNEATEMPNTIRY 368

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 54001 seqs, 7132810 residues

Total number of hits satisfying chosen parameters: 54001

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New.\*  
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4: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
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6: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	887	45.4	379	7	US-11-109-156-16
2	878	45.0	360	6	US-10-878-556A-134
3	878	45.0	360	7	US-11-186-284-115
4	747.5	38.3	365	6	US-10-770-726-69
5	653	33.4	422	6	US-10-857-780-21
6	518	26.5	292	6	US-10-770-726-53
7	491.5	25.2	496	6	US-10-770-726-72
8	467.5	23.9	298	6	US-10-770-726-51
9	461	23.6	346	6	US-10-770-726-55
10	457	23.4	297	6	US-10-770-726-48
11	457	23.4	297	7	US-11-109-156-11
12	440	22.5	433	6	US-10-770-726-65
13	438	22.4	483	6	US-10-451-375-12
14	435.5	22.3	795	6	US-10-770-726-49
15	434.5	22.2	303	6	US-10-770-726-52
16	433	22.2	256	7	US-11-113-424-183
17	349.5	17.9	391	6	US-10-770-726-59
18	321.5	16.5	355	6	US-10-451-375-2
19	321.5	16.5	457	6	US-10-451-375-6
20	313.5	16.1	1162	6	US-10-451-375-3
21	312.5	16.0	1198	6	US-10-451-375-4
22	305	15.6	333	7	US-11-004-789-2
23	305	15.6	334	7	US-11-111-239-4
24	296	15.2	318	7	US-11-109-156-15
25	296	15.2	1133	6	US-10-821-234-1219

26 295.5 15.1 318 7 US-11-111-239-2  
27 286 14.6 970 6 US-10-770-726-86  
28 279 14.3 275 6 US-10-523-477-10  
29 277.5 14.2 603 6 US-10-770-726-75  
30 274 14.0 433 7 US-11-109-156-9  
31 273 14.0 591 6 US-10-770-726-71  
32 271.5 13.9 403 6 US-10-523-477-11  
33 271.5 13.9 403 6 US-10-770-726-83  
34 271.5 13.9 403 6 US-10-770-726-85  
35 271.5 13.9 403 7 US-11-109-156-12  
36 271.5 13.9 403 7 US-11-092-168-1  
37 270 13.8 540 7 US-11-099-691-2  
38 269.5 13.8 766 6 US-10-821-234-1691  
39 268.5 13.7 651 6 US-10-770-726-67  
40 266.5 13.6 471 6 US-10-770-726-68  
41 263.5 13.5 740 6 US-10-878-556A-129  
42 263 13.3 332 6 US-10-497-767-3  
43 260 13.3 348 6 US-10-661-426-12  
44 256 13.1 445 6 US-10-770-726-70  
45 255.5 13.1 366 6 US-10-661-426-7

## ALIGNMENTS

RESULT 1  
US-11-109-156-16  
; Sequence 16, Application US/1109156  
; Publication No. US20050250144A1  
; GENERAL INFORMATION:  
; APPLICANT: Toshio Ota  
; APPLICANT: Takao Isogai  
; APPLICANT: Tetsuo Nishikawa  
; APPLICANT: Koji Hayashi  
; APPLICANT: Kaoru Otsuka  
; APPLICANT: Jun-ichi Yamamoto  
; APPLICANT: Shizuko Ishii  
; APPLICANT: Tomoyasu Sugiyama  
; APPLICANT: Ai Wakamatsu  
; APPLICANT: Keiichi Nagai  
; APPLICANT: Tetsuji Otsuki  
; APPLICANT: Shin-ichi Funahashi  
; APPLICANT: Chiaki Senoo  
; APPLICANT: Jun-ichi Nezu  
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN PHOSPHATASE  
; FILE REFERENCE: 06501-099002  
; CURRENT APPLICATION NUMBER: US/11/109,156  
; PRIOR FILING DATE: 2005-04-19  
; PRIOR APPLICATION NUMBER: US/10/060,065  
; PRIOR FILING DATE: 2002-01-29  
; PRIOR APPLICATION NUMBER: PCT/JP00/05061  
; PRIOR FILING DATE: 2000-07-28  
; PRIOR APPLICATION NUMBER: US 60/159,590  
; PRIOR FILING DATE: 1999-10-18  
; PRIOR APPLICATION NUMBER: US 60/183,322  
; PRIOR FILING DATE: 2000-02-17  
; PRIOR APPLICATION NUMBER: JP 11-248036  
; PRIOR FILING DATE: 1999-07-29  
; PRIOR APPLICATION NUMBER: JP 2000-118776  
; PRIOR APPLICATION NUMBER: JP 2000-183767  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: JP 2000-241899  
; PRIOR FILING DATE: 2000-06-09  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 379  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-109-156-16

Sequence 2, Appli  
Sequence 86, Appl  
Sequence 10, Appl  
Sequence 9, Appli  
Sequence 71, Appl  
Sequence 11, Appl  
Sequence 83, Appl  
Sequence 85, Appl  
Sequence 12, Appl  
Sequence 1, Appli  
Sequence 2, Appli  
Sequence 1691, Ap  
Sequence 67, Appl  
Sequence 68, Appl  
Sequence 129, App  
Sequence 3, Appli  
Sequence 12, Appl  
Sequence 70, Appl  
Sequence 7, Appli

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Query Match 45.4%; Score 887; DB 7; Length 379;
Best Local Similarity 50.0%; Pred. No. 4.6e-70;
Matches 173; Conservative 65; Mismatches 100; Indels 8; Gaps 5;

QY 26 GNKFVYTKYQPPIMPGRGAYGIVCSVMNFETREMAIKKIANAFNNDMDAKRTILREIK 85
DB 33 GQFVDVGPRY-TQLQVIGEGAYGMVSSAYDNVNRKTRVAIKKI-SPEHQTYCQRTILREIQ 90

QY 86 LLRHLDHENIIGIRDVIPPPIQAFNDVYIATLMDTLHIIIRSNQELSEBHCQYFLYQ 145
DB 91 LLRPFHENIIGINDIRAPTIEQMKDVIYVQDLMETDLYKLLKT-QHLSNDHICYFLYQ 149

QY 146 ILRGLKYIHSANVHRDLKPSNLLNANCDLKICDFGLARPS-SSSDMMTEYVYVTRW 201
DB 150 ILRGLKYIHSANVLRDLKPSNLLNTTCDLKICDFGLARVADPDHDHTGFLTEYVATRW 209

QY 202 YRAPELLLNSTDYS-AADVWSVGCIFMELINRQPLFGCRDHMHQMLITEVIGTPTDDEL 260
DB 210 YRAPEIMLNSKGYTSIDISWVGCILAEMLSNRPIFGKHLYDLQNLHILGILGSPSQEDL 269

QY 261 GFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIERMLTFNPLQRTIVVEALDHPY 320
DB 270 NCIIINKARNYLSLSPHKNKVPWNLFNPNADSKALDLDKMLTFNPKHRIEVEQALAHFY 329

QY 321 LERLHDIADPEICLPFFSDFEQKALNEDQMKQLIFNEAIEAENPNIR 366
DB 330 LEQYDPTDEPVAEEPTFAMELDDLPKEKLKELIFEETARFQPGV 375

RESULT 2
US-10-878-556A-134
; Sequence 134, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 134
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: sw_hum/mk01_human
; DATABASE ENTRY DATE: 1992-12-01
US-10-878-556A-134

Query Match 45.0%; Score 878; DB 6; Length 360;
Best Local Similarity 50.1%; Pred. No. 2.6e-69;
Matches 174; Conservative 61; Mismatches 104; Indels 8; Gaps 5;

QY 26 GNKFVYTKYQPPIMPGRGAYGIVCSVMNFETREMAIKKIANAFNNDMDAKRTILREIK 85
DB 16 GQFVDVGPRY-TNLSYIGEGAYGMVCSAYDNVNRKTRVAIKKI-SPEHQTYCQRTILREIK 73

QY 86 LLRHLDHENIIGIRDVIPPPIQAFNDVYIATLMDTLHIIIRSNQELSEBHCQYFLYQ 145
DB 74 LLRPFHENIIGINDIRAPTIEQMKDVIYVQDLMETDLYKLLKT-QHLSNDHICYFLYQ 132

QY 146 ILRGLKYIHSANVHRDLKPSNLLNANCDLKICDFGLARPS-SSSDMMTEYVYVTRW 201
DB 133 ILRGLKYIHSANVLRDLKPSNLLNTTCDLKICDFGLARVADPDHDHTGFLTEYVATRW 192

QY 202 YRAPELLLNSTDYS-AADVWSVGCIFMELINRQPLFGCRDHMHQMLITEVIGTPTDDEL 260
DB 193 YRAPEIMLNSKGYTSIDISWVGCILAEMLSNRPIFGKHLYDLQNLHILGILGSPSQEDL 252

QY 261 GFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIERMLTFNPLQRTIVVEALDHPY 320
DB 253 NCIIINKARNYLSLSPHKNKVPWNLFNPNADSKALDLDKMLTFNPKHRIEVEQALAHFY 312

QY 321 LERLHDIADPEICLPFFSDFEQKALNEDQMKQLIFNEAIEAENPNIR 367
DB 330 LEQYDPTDEPVAEEPTFAMELDDLPKEKLKELIFEETARFQPGV 359

RESULT 4
US-10-770-726-69
; Sequence 69, Application US/10770726
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QY 321 LERLHDIADPEICLPFFSDFEQKALNEDQMKQLIFNEAIEAENPNIR 367
DB 330 LEQYDPTDEPVAEEPTFAMELDDLPKEKLKELIFEETARFQPGV 359

RESULT 3
US-11-186-284-115
; Sequence 115, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MP001-0292P2RMN
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 115
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-115

Query Match 45.0%; Score 878; DB 7; Length 360;
Best Local Similarity 50.1%; Pred. No. 2.6e-69;
Matches 174; Conservative 61; Mismatches 104; Indels 8; Gaps 5;

QY 26 GNKFVYTKYQPPIMPGRGAYGIVCSVMNFETREMAIKKIANAFNNDMDAKRTILREIK 85
DB 16 GQFVDVGPRY-TNLSYIGEGAYGMVCSAYDNVNRKTRVAIKKI-SPEHQTYCQRTILREIK 73

QY 86 LLRHLDHENIIGIRDVIPPPIQAFNDVYIATLMDTLHIIIRSNQELSEBHCQYFLYQ 145
DB 74 LLRPFHENIIGINDIRAPTIEQMKDVIYVQDLMETDLYKLLKT-QHLSNDHICYFLYQ 132

QY 146 ILRGLKYIHSANVHRDLKPSNLLNANCDLKICDFGLARPS-SSSDMMTEYVYVTRW 201
DB 133 ILRGLKYIHSANVLRDLKPSNLLNTTCDLKICDFGLARVADPDHDHTGFLTEYVATRW 192

QY 202 YRAPELLLNSTDYS-AADVWSVGCIFMELINRQPLFGCRDHMHQMLITEVIGTPTDDEL 260
DB 193 YRAPEIMLNSKGYTSIDISWVGCILAEMLSNRPIFGKHLYDLQNLHILGILGSPSQEDL 252

QY 261 GFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIERMLTFNPLQRTIVVEALDHPY 320
DB 253 NCIIINKARNYLSLSPHKNKVPWNLFNPNADSKALDLDKMLTFNPKHRIEVEQALAHFY 312

QY 321 LERLHDIADPEICLPFFSDFEQKALNEDQMKQLIFNEAIEAENPNIR 367
DB 330 LEQYDPTDEPVAEEPTFAMELDDLPKEKLKELIFEETARFQPGV 359

RESULT 4
US-10-770-726-69
; Sequence 69, Application US/10770726
```





RESULT 10  
 US-10-770-726-48  
 ; Sequence 48, Application US/10770726  
 ; Publication No. US20050266409A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wyeth  
 ; APPLICANT: Brown, Eugene  
 ; APPLICANT: Liu, Wei  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING  
 ; TITLE OF INVENTION: CANCERS  
 ; FILE REFERENCE: AW101079 (031896-010000)  
 ; CURRENT APPLICATION NUMBER: US/10/770,726  
 ; CURRENT FILING DATE: 2004-02-04  
 ; NUMBER OF SEQ ID NOS: 48640  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 48  
 ; LENGTH: 297  
 ; TYPE: prt  
 ; ORGANISM: Homo sapiens  
 US-10-770-726-48







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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 27, 2005, 20:33:21 ; Search time 164 Seconds  
(without alignments)  
937.568 Million cell updates/sec

Title: US-10-768-886-2  
Perfect score: 1953  
Sequence: 1 MDGAPVAEPRPTWTHGGRYL.....DQMKQLIFNEAEMPNIRY 368

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.Main:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
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6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1953	100.0	368	4	US-10-768-886-2
2	1819.5	93.2	369	5	US-10-732-923-1342
3	1775.5	90.9	397	4	US-10-425-115-191397
4	1682.5	86.1	374	4	US-10-767-701-45777
5	1476.5	75.6	376	5	US-10-732-923-1332
6	1461.5	74.8	375	5	US-10-732-923-1324
7	1448.5	74.2	396	5	US-10-732-923-1446
8	1437.5	73.6	394	5	US-10-732-923-1447
9	1436.5	73.6	393	5	US-10-732-923-1331
10	1430	73.2	365	5	US-10-732-923-1334
11	1421.5	72.8	394	5	US-10-732-923-1323
12	1340.5	68.6	318	4	US-10-424-599-284784
13	1340.5	68.6	318	4	US-10-425-114-49119
14	1334.5	68.3	266	4	US-10-768-886-4
15	1331.5	68.2	377	4	US-10-767-701-45781
16	1331.5	68.2	403	4	US-10-425-114-67488
17	1325.5	67.9	372	4	US-10-425-115-271614
18	1325.5	67.9	380	4	US-10-425-114-67200
19	1323	67.7	395	4	US-10-437-963-137817
20	1322.5	67.7	376	4	US-10-437-963-139244
21	1316.5	67.4	376	3	US-09-730-478A-2
22	1310.5	67.1	417	5	US-10-732-923-1280
23	1295.5	66.3	379	5	US-10-732-923-1448
24	1260.5	64.5	375	3	US-09-828-313-34
25	1260.5	64.5	375	4	US-10-768-863A-34
26	1232.5	63.1	373	5	US-10-739-930-10557
27	1090.5	55.8	295	4	US-10-767-701-43229

28	1074.5	55.0	216	4	US-10-425-114-42499	Sequence 42499, A
29	1012	51.8	369	4	US-10-767-701-42772	Sequence 42772, A
30	1003.5	51.4	370	5	US-10-739-930-10966	Sequence 10966, A
31	995	50.9	370	4	US-10-767-701-45385	Sequence 45385, A
32	993	50.8	247	4	US-10-425-114-55085	Sequence 55085, A
33	987.5	50.6	372	4	US-10-425-114-62386	Sequence 62386, A
34	985.5	50.5	480	4	US-10-168-844-9	Sequence 9, Appli
35	985	50.4	368	5	US-10-732-923-1302	Sequence 1302, Ap
36	982	50.3	370	4	US-10-342-224-104	Sequence 104, App
37	981	50.2	368	5	US-10-739-930-6166	Sequence 6166, Ap
38	965	49.4	369	4	US-10-424-599-177815	Sequence 177815,
39	949.5	48.6	227	4	US-10-424-599-284783	Sequence 284783,
40	933.5	47.8	354	5	US-10-732-923-1366	Sequence 1366, Ap
41	932	47.7	371	5	US-10-739-930-10965	Sequence 10965, A
42	929	47.6	371	4	US-10-424-599-206406	Sequence 206406,
43	927	47.5	353	5	US-10-732-923-1492	Sequence 1492, Ap
44	926.5	47.4	261	4	US-10-425-115-350696	Sequence 350696,
45	925.5	47.4	308	4	US-10-425-115-350699	Sequence 350699,

ALIGNMENTS

RESULT 1  
US-10-768-886-2  
; Sequence 2, Application US/10768886  
; Publication No. US20040209325A1  
; GENERAL INFORMATION:  
; APPLICANT: Board of Trustees for University of Arkansas  
; TITLE OF INVENTION: Mitogen-Activated Protein Kinase and Method of Use to Enhance  
; TITLE OF INVENTION: Biotic and Abiotic Stress Tolerance in Plants  
; FILE REFERENCE: UAP-03-14  
; CURRENT APPLICATION NUMBER: US/10/768,886  
; CURRENT FILING DATE: 2004-01-31  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2  
; LENGTH: 368  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-10-768-886-2

Query Match 100.0%; Score 1953; DB 4; Length 368;  
Best Local Similarity 100.0%; Pred. No. 7.1e-153;  
Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MDGAPVAEPRPTWTHGGRYLLYDIFGNKFEVTKYQPPIMPICRGAYGIVCSVMNPETRE	60
DB	1	MDGAPVAEPRPTWTHGGRYLLYDIFGNKFEVTKYQPPIMPICRGAYGIVCSVMNPETRE	60
QY	61	MVAIKKIANAFNNDMAKRTLRKILRLDHNHNIIGIRDVIPPPIPOAFNDVYIATELM	120
DB	61	MVAIKKIANAFNNDMAKRTLRKILRLDHNHNIIGIRDVIPPPIPOAFNDVYIATELM	120
QY	121	DTDLHHIIRSNQELSEHCQFLYQLRGKYTHSANVHRDLKPSNLLNANCDLKICD	180
DB	121	DTDLHHIIRSNQELSEHCQFLYQLRGKYTHSANVHRDLKPSNLLNANCDLKICD	180
QY	181	FGLARPSSESDMMTEVTVTRWYRAPPELLNLSNTDYSAADVMSVGCIFMELINRPLPFGRD	240
DB	181	FGLARPSSESDMMTEVTVTRWYRAPPELLNLSNTDYSAADVMSVGCIFMELINRPLPFGRD	240
QY	241	HHQMELITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPRPVQPAALDLIER	300
DB	241	HHQMELITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPRPVQPAALDLIER	300
QY	301	MLTFNPLQRIITVEALDHPYLERLHDIADPEICLPSFDFEQKALNEDQMKLIIFNEAI	360
DB	301	MLTFNPLQRIITVEALDHPYLERLHDIADPEICLPSFDFEQKALNEDQMKLIIFNEAI	360
QY	361	EMNPNIY 368	
DB	361	EMNPNIY 368	

```
RESULT 2
US-10-732-923-1342
; Sequence 1342, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 1342
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Avena sativa
US-10-732-923-1342

Query Match      93.2%; Score 1819.5; DB 5; Length 369;
Best Local Similarity 91.3%; Pred. No. 7.5e-142;
Matches 337; Conservative 20; Mismatches 11; Indels 1; Gaps 1;

QY 1 MDGAPVAEFPRTMTGGRYLLYDIFGNKPEVTNKYQPPIMPPIGRGAYGIVCSVMNFETRE 60
DB 1 MDGAPVAEFPRTMTGGRFLLYNIFGNQFEITSKYQPPIMPPIGRGAYGIVCSVMNFETRE 60
QY 61 MVAIKKIANAFNNDMDAKRTLRKILRLHLDHENIIGIRDVIPPPIQAFNDVYIATELM 120
DB 61 MVAIKKIANAFNNDMDAKRTLRKILRLHLDHENIIVGLRDVIPPPIQSFNDVYIATELM 120
QY 121 DTDLHHIIRSNQELSEHCQYFLYQLRGLKYTHSANVIHRDLKPSNLLNANCDLKICD 180
DB 121 DTDLHHIIRSNQELSEHCQYFLYQLRGLKYTHSANVIHRDLKPSNLLNANCDLKICD 180
QY 181 FGLARPSSESDMTTEYVTVRWYRAPELLLNSTDYSAADVMSVGCIFMELINRQPLFPGR 239
DB 181 FGLARPSSESDMTTEYVTVRWYRAPELLLNSTDYSAADVMSVGCIFMELINRQPLFPGR 240
QY 240 DHMHQRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIE 299
DB 241 DHMHQRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIE 300
QY 300 RMLTFNPLQRTITVEEALDHPYLERLHDADEPCTDFFSFQHPFLTEQMKQLIFNEA 359
DB 301 RMLTFNPLQRTITVEEALDHPYLERLHDADEPCTDFFSFQHPFLTEQMKQLIFNEA 360
QY 360 IEMNPRIY 368
DB 361 LELNPNRY 369

RESULT 3
US-10-425-115-191397
; Sequence 191397, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 191397
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Zea mays

Query Match      86.1%; Score 1682.5; DB 4; Length 374;
Best Local Similarity 87.3%; Pred. No. 1.6e-130;
Matches 322; Conservative 15; Mismatches 15; Indels 1; Gaps 1;

QY 1 MDGAPVAEFPRTMTGGRYLLYDIFGNKPEVTNKYQPPIMPPIGRGAYGIVCSVMNFETRE 60
DB 6 MDGAPVAEFPRTVTHNGFLQYINIFGNLFEITHKYQPPIMPPIGRGAYGIVCSVMNFETRE 65
QY 61 MVAIKKIANAFNNDMDAKRTLRKILRLHLDHENIIGIRDVIPPPIQAFNDVYIATELM 120
DB 61 MVAIKKIANAFNNDMDAKRTLRKILRLHLDHENIIVGLRDVIPPPIQSFNDVYIATELM 120
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; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(397)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_106134C.1.pep
US-10-425-115-191397

Query Match      90.9%; Score 1775.5; DB 4; Length 397;
Best Local Similarity 84.4%; Pred. No. 3.5e-138;
Matches 335; Conservative 20; Mismatches 13; Indels 29; Gaps 2;

QY 1 MDGAPVAEFPRTMTGGRYLLYDIFGNKPEVTNKYQPPIMPPIGRGAYGIVCSVMNFETRE 60
DB 1 MDGAPVAEFPRTMTGGRFLLYNIFGNQFEITAKYQPPIMPPIGRGAYGIVCSVMNFETRE 60
QY 61 MVAIKKIANAFNNDMDAKRTLRKILRLHLDHENIIGIRDVIPPPIQAFNDVYIATELM 120
DB 61 MVAIKKIANAFNNDMDAKRTLRKILRLHLDHENIIVGLRDVIPPPIQSFNDVYIATELM 120
QY 121 DTDLHHIIRSNQELSEHCQYFLYQLRGLKYTHSANVIHRDLKPSNLLNANCDLKICD 180
DB 121 DTDLHHIIRSNQELSEHCQYFLYQLRGLKYTHSANVIHRDLKPSNLLNANCDLKICD 180
QY 181 FGLARPSSESDMTTEYVTVRWYRAPELLLNSTDYSAADVMSVGCIFMELINRQPLFPGR 239
DB 181 FGLARPSSESDMTTEYVTVRWYRAPELLLNSTDYSAADVMSVGCIFMELIDRRPLFPGR 240
QY 240 DHMHQRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIE 299
DB 241 DHMHQRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPFRVQPLVLDLIE 300
QY 300 RMLTFNPLQRTITVEEALDHPYLERLHDADEPCTDFFSFQHPFLTEQMKQLIFNEA 331
DB 301 RMLTFNPLQRTITVTVHWHGGRFRPRTSHRDLFCBAVAALAHPLYERLHDADEPCTDFFSFQHPFLTEQMKQLIFNEA 360
QY 332 ICLEPFSDFEQKALNEDQMKQLIFNEAIEEMNPRIY 368
DB 361 VCTEPFSDFEQKALNEDQMKQLIFNEAIEELNPSRY 397

RESULT 4
US-10-767-701-45777
; Sequence 45777, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 45777
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C35159_1.pep
US-10-767-701-45777

Query Match      86.1%; Score 1682.5; DB 4; Length 374;
Best Local Similarity 87.3%; Pred. No. 1.6e-130;
Matches 322; Conservative 15; Mismatches 15; Indels 1; Gaps 1;

QY 1 MDGAPVAEFPRTMTGGRYLLYDIFGNKPEVTNKYQPPIMPPIGRGAYGIVCSVMNFETRE 60
DB 6 MDGAPVAEFPRTVTHNGFLQYINIFGNLFEITHKYQPPIMPPIGRGAYGIVCSVMNFETRE 65
QY 61 MVAIKKIANAFNNDMDAKRTLRKILRLHLDHENIIGIRDVIPPPIQAFNDVYIATELM 120
DB 61 MVAIKKIANAFNNDMDAKRTLRKILRLHLDHENIIVGLRDVIPPPIQSFNDVYIATELM 120
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Db 66 MVAIKKIANAFNDHMDAKRTLRKILRLHLDHENIIGIRDVIPPPIQAFNDVYIGTEL 125  
 QY 121 DTDLHHIIRSNQELSEHCQFYQILRLGLKYIHSANVIRDLKPSNLLNANCDLKICD 180  
 Db 126 DTDLHHIIRSNQELSEHCQFYQILRLGLKYIHSANVIRDLKPSNLLNANCDLKICD 185  
 QY 181 FGLARPSSEDMTEYVVRWYRAPELLNSTDYSA-DVWSVGCIFMELINRQPLPPGR 239  
 Db 186 VAKNTAYACDMTEYVVRWYRAPELLNSTDYSAIDVWSVGCIFMELINRQPLPPGR 245  
 QY 240 DHMHOMRLITEVIGTPTDDELGRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIE 299  
 Db 246 DHMHOMRLITEVIGTPTDDELGRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIE 305  
 QY 300 RMLTFNPLQRIITVEALDHPYLERLHDADEPICLPPFSDFEQKALNEDQKQILFNEA 359  
 Db 306 RMLTFNPLQRIITVEALDHPYLERLHDADEPICLPPFSDFEQKALNEDQKQILFNEA 365  
 QY 360 IENNPNIY 368  
 Db 366 IENNPNIY 374

## RESULT 5

US-10-732-923-1332  
 ; Sequence 1332, Application US/10732923  
 ; Publication No. US20050108791A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Edgerton, Michael D  
 ; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES  
 ; FILE REFERENCE: 38-15(52796)C  
 ; CURRENT APPLICATION NUMBER: US/10/732,923  
 ; CURRENT FILING DATE: 2003-12-10  
 ; PRIOR APPLICATION NUMBER: 10/310,154  
 ; PRIOR FILING DATE: 2002-12-04  
 ; NUMBER OF SEQ ID NOS: 24149  
 ; SEQ ID NO 1332  
 ; LENGTH: 376  
 ; TYPE: PRT  
 ; ORGANISM: Nicotiana benthamiana  
 US-10-732-923-1332

Query Match 75.6%; Score 1476.5; DB 5; Length 376;  
 Best Local Similarity 72.7%; Pred. No. 1.6e-113;  
 Matches 264; Conservative 57; Mismatches 41; Indels 1; Gaps 1;  
 QY 3 GAPVAFPRPTMTGGRYLLYDIFGNKFEVTKYQPPIMPGRGAYGIVCSVMNPFETREMV 62  
 Db 11 GQGFPPPSVLTGGQYVQYDIFGNFFETTKYRPPIMPGRGAYGIVCSVLTNEMV 70  
 QY 63 AIKKIANAFNDMDAKRTLRKILRLHLDHENIIGIRDVIPPPIQAFNDVYIATLMDT 122  
 Db 71 AVKIANAFNDYMDAKRTLRKILRLHLDHENIIGIRDVIPPPLRRREFSDVYIATLMDT 130  
 QY 123 DLHHIIRSNQELSEHCQFYQILRLGLKYIHSANVIRDLKPSNLLNANCDLKICDFG 182  
 Db 131 DLHQIIRSNQGLSEHCHQYFMYQLRLGLKYIHSANVIRDLKPSNLLNANCDLKICDFG 190  
 QY 183 LARPSSEDMTEYVVRWYRAPELLNSTDYSA-DVWSVGCIFMELINRQPLPPGRDH 241  
 Db 191 LARPNTENEMTEYVVRWYRAPELLNSTDYTAIDVWSVGCIFMELMNRKELFAGKH 250  
 QY 242 MHQMRLLITEVIGTPTDDELGRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIERM 301  
 Db 251 VHQIRLLTELLGPTTEADIGFLQNEADAKYIRQLPQHPROQLANVFPVFNPLAIDLVDKM 310  
 QY 302 LTFNPLQRIITVEALDHPYLERLHDADEPICLPPFSDFEQKALNEDQKQILFNEAIE 361  
 Db 311 LTLDPTRITVEALDHPYLERLHDADEPICVPPSSDFEQQIGSEQIKDMYQEALS 370  
 QY 362 MNP 364  
 Db 371 LNP 373

## RESULT 6

US-10-732-923-1324  
 ; Sequence 1324, Application US/10732923  
 ; Publication No. US20050108791A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Edgerton, Michael D  
 ; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES  
 ; FILE REFERENCE: 38-15(52796)C  
 ; CURRENT APPLICATION NUMBER: US/10/732,923  
 ; CURRENT FILING DATE: 2003-12-10  
 ; PRIOR APPLICATION NUMBER: 10/310,154  
 ; PRIOR FILING DATE: 2002-12-04  
 ; NUMBER OF SEQ ID NOS: 24149  
 ; SEQ ID NO 1324  
 ; LENGTH: 375  
 ; TYPE: PRT  
 ; ORGANISM: Capsicum annuum  
 US-10-732-923-1324

Query Match 74.8%; Score 1461.5; DB 5; Length 375;  
 Best Local Similarity 72.7%; Pred. No. 2.8e-112;  
 Matches 264; Conservative 52; Mismatches 46; Indels 1; Gaps 1;  
 QY 3 GAPVAFPRPTMTGGRYLLYDIFGNKFEVTKYQPPIMPGRGAYGIVCSVMNPFETREMV 62  
 Db 10 GQGFPPFNIVTHGGQYVQYDIFGNFFETTKYRPPIMPGRGAYGIVCSVFNELNEMV 69  
 QY 63 AIKKIANAFNDMDAKRTLRKILRLHLDHENIIGIRDVIPPPIQAFNDVYIATLMDT 122  
 Db 70 AVKIANAFNDYMDAKRTLRKILRLHLDHENIIGIRDVIPPPLRRREFSDVYIATLMDT 129  
 QY 123 DLHHIIRSNQELSEHCQFYQILRLGLKYIHSANVIRDLKPSNLLNANCDLKICDFG 182  
 Db 130 DLHQIIRSNQGLSEHCHQYFMYQLRLGLKYIHSANVIRDLKPSNLLNANCDLKICDFG 189  
 QY 183 LARPSSEDMTEYVVRWYRAPELLNSTDYS-AADVWSVGCIFMELINRQPLPPGRDH 241  
 Db 190 LARPNTENEMTEYVVRWYRAPELLNSTDYTAIDVWSVGCIFMELMNRKELFAGKH 249  
 QY 242 MHQMRLLITEVIGTPTDDELGRNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIERM 301  
 Db 250 VHQIRLLTELLGPTTESDLSFLRNEDAKYIRQLPQHPROQLAKVPFHVNSLAIELVDKM 309  
 QY 302 LTFNPLQRIITVEALDHPYLERLHDADEPICLPPFSDFEQKALNEDQKQILFNEAIE 361  
 Db 310 LTLNPTGRITVEALAHAPYLAKLHDAADPVCVPFSDFEQQIGSEQIKDMYQEALV 369  
 QY 362 MNP 364  
 Db 370 LNP 372

## RESULT 7

US-10-732-923-1446  
 ; Sequence 1446, Application US/10732923  
 ; Publication No. US20050108791A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Edgerton, Michael D  
 ; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES  
 ; FILE REFERENCE: 38-15(52796)C  
 ; CURRENT APPLICATION NUMBER: US/10/732,923  
 ; CURRENT FILING DATE: 2003-12-10  
 ; PRIOR APPLICATION NUMBER: 10/310,154  
 ; PRIOR FILING DATE: 2002-12-04  
 ; NUMBER OF SEQ ID NOS: 24149  
 ; SEQ ID NO 1446  
 ; LENGTH: 396  
 ; TYPE: PRT  
 ; ORGANISM: Solanum tuberosum  
 US-10-732-923-1446

Query Match	74.2%;	Score 1448.5;	DB 5;	Length 396;	
Best Local Similarity	73.7%;	Pred. No. 3.5e-111;			
Matches 269;	Conservative 48;	Mismatches 41;	Indels 7;	Gaps 3	
1	MDGAVASFRPMTWGGRRLLYDI	FGNKPEVTNKPQPPIMPIGRGAYGIVCSVMVFETRE	60		
33	MDNIFA-----TLHGGRFIQNI	FGNIFEVTAQYKPPIMPLGKAGYGIVCSALNSETNE	87		
61	MVAIKKIANAFNDMDAKRTLEIK	LLRLHDHENIIGIRDVTPPIPOAFNDVVIATETLM	120		
88	NVAIKKIANAFONKIDAKRTLEIK	LLRHMHDENIVAIRDIIPPPQREAFNDVVIATETLM	147		
121	DTDLHHIIRSNQELSEEHCOYFL	YQILGKLYIHSANVTHRDLKPSNLLLNANCDLKICD	180		
148	DTDLHQIIRSNQGLSEEHCOYFL	YQLRGKLYIHSANVTHRDLKPSNLLLNANCDLKICD	207		
181	FGLARPSSESMDMTYVVTWTRAP	PELLNSTDYSA--DVWSVGCI FMELINRQPLFPCR	239		
208	FGLARVTSETDPMTEYVVTWTR	YRYPPELLNSSDYTAADVWSVGCI FMELMDRKPLFPCR	267		
240	DMHQVRLITEVIGTPTDDELGFI	RNEDARKTWRLHPQYPRTPFASMPPRVOPAAIDLIE	299		
268	DHVHQRLIMELIGTPEASEMEFL	-NENAKRYIQLPYLRQSPTKEPHVNPAAIDLVE	326		
300	RMLTFNPQRITVBEALDHPYLER	LHDADBEPCLEPFSDFEQKALNEDOMKOLIFNEA	359		
327	KMLTFDPRRITVEDALAHPYLA	SLHDISEDFICMTFPNDFEQALTEQMKELIYRES	386		
360	TEMNP	364			
387	IAFNP	391			

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RESULT 8
US-10-732-923-1447
; Sequence 1447, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 1447
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Solanum tuberosum
US-10-732-923-1447

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Db      266  DHVHQURLLMELGTSPSEAMEBFL-NENAKRYIRQLPLYRQSFVEKFPHVNPAAIDLVE 324
Qy      300  RMLTFNPLQKITVEEALDHPYLERLHDIADEPICLEPPFSFDFEQKALNEDQMKQLIFNEA 359
Db      325  KMLTFPDRRLTVEGALAHPLYLTSLHDISDEPVCMTFFSDFDEQHALTEQMKELLYREG 384
Qy      360  IEMNPNIRY 368
Db      385  LAFNPEYQH 393

RESULT 9
US-10-732-923-1331
; Sequence 1331, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 1331
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Nicotiana benthamiana
US-10-732-923-1331

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RESULT 10  
US-10-732-923-1334  
; Sequence 1334, Application US/10732923  
; Publication No. US20050108791A1  
; GENERAL INFORMATION:  
; APPLICANT: Edgerton, Michael D  
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES  
; FILE REFERENCE: 38-15 (52796)C  
; CURRENT APPLICATION NUMBER: US/10/732,923







Db 251 IQQLTELIGSPDDASLGLRSDNAKRYMKQLPOFFRODFRLRFNNMFGAVDLDERM 310  
Qy 302 LTFNPLQRITVBEALDHPYLERLHDIADEPICLEPFPSFDFEQKALNEDQMKQLIFNEAIE 361  
Db 311 LVFDPSSRRITVDEALHHPYLASLHDINEEPTCPAPFSFDFEQPSFTEAHIKELIWRESLA 370  
Qy 362 MNPNIY 368  
Db 371 FNPDPY 377

Search completed: December 27, 2005, 20:44:50  
Job time : 166 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2005, 20:33:06 ; Search time 46 Seconds  
(without alignments)

661.405 Million cell updates/sec

Title: US-10-768-886-2

Perfect score: 1953  
Sequence: 1 MDGAPVAFRPTTHGGRYL.....DOMKQLIFNEAIEPNIRY 368

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA,\*  
1: /cgm2\_6/ptodata/1/iaa/5 COMB.pep.\*  
2: /cgm2\_6/ptodata/1/iaa/6 COMB.pep.\*  
3: /cgm2\_6/ptodata/1/iaa/H COMB.pep.\*  
4: /cgm2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*  
5: /cgm2\_6/ptodata/1/iaa/RE COMB.pep.\*  
6: /cgm2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1504.5	77.0	371	1	US-08-837-593-6
2	1472.5	75.4	375	1	US-08-837-593-5
3	1472.5	75.4	375	2	US-09-623-034-2
4	1471.5	75.3	370	1	US-08-837-593-7
5	1448	74.1	387	1	US-08-837-593-4
6	1445.5	74.0	393	1	US-08-837-593-3
7	1438.5	73.7	393	1	US-08-837-593-2
8	1327.5	68.0	371	1	US-08-837-593-8
9	1260.5	64.5	375	2	US-09-828-313-34
10	1031	52.8	372	1	US-08-837-593-9
11	921.5	47.2	304	2	US-09-739-455-13
12	921.5	47.2	304	2	US-09-739-455-23
13	921.5	47.2	304	2	US-10-153-919-13
14	921.5	47.2	304	2	US-10-153-919-23
15	904	46.3	624	2	US-09-417-197-57
16	902	46.2	365	1	US-08-176-620A-2
17	902	46.2	365	1	US-08-463-862-2
18	902	46.2	365	1	US-08-461-985-2
19	902	46.2	365	1	US-08-458-887-2
20	902	46.2	365	2	US-08-932-787B-2
21	902	46.2	365	2	US-08-932-012C-2
22	902	46.2	365	2	US-08-888-818C-2
23	902	46.2	367	1	US-08-176-620A-11
24	902	46.2	367	1	US-08-461-985-11
25	896	45.9	353	1	US-08-176-620A-14
26	896	45.9	353	1	US-08-461-985-14
27	894	45.8	353	2	US-09-487-558B-116

Sequence 8, Appli  
Sequence 8, Appli  
Sequence 14, Appli  
Sequence 1021, Ap  
Sequence 25, Appli  
Sequence 25, Appli  
Sequence 39, Appli  
Sequence 9, Appli  
Sequence 8, Appli  
Sequence 9919, Ap  
Sequence 3, Appli  
Sequence 1028, Ap  
Sequence 12, Appli  
Sequence 4, Appli  
Sequence 14, Appli

## ALIGNMENTS

### RESULT 1

US-08-837-593-6  
; Sequence 6, Application US/08837593  
; Patent No. 5977442  
; GENERAL INFORMATION:  
; APPLICANT: Klessig, Daniel F.  
; TITLE OF INVENTION: "No. 5977442el Salicylic Acid Induced  
; TITLE OF INVENTION: Map Kinase and its Use for Enhanced Disease Resistance in Pla  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman,  
; ADDRESSEE: P.C.  
; STREET: 1601 Market Street, Suite 720  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: United States of America  
; ZIP: 19103-2307  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/837,593  
; FILING DATE: April 21, 1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/029,805  
; FILING DATE: October 25, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Reed, Janet E.  
; REGISTRATION NUMBER: 36,252  
; REFERENCE/DOCKET NUMBER: Rutgers 97-0016  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 563-4100  
; TELEFAX: (215) 563-4044  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 371 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
; US-08-837-593-6



QY 63 AIKKIANAFNDMDAKRTLEIKLRLHLDHENIIGIRVDVPPPIPOAFNDVYIATLMDT 122  
Db 70 AVKKIANAFDIYNDAKRTLEIKLRLHLDHENIIGIRVDVPPPIRREFSDVYIATLMDT 129  
QY 123 DLHIIIRSNQBLSEHCQYFLYQILRLGLKYIHSANVIHRDLKPSNLLNANCDLKICDFG 182  
Db 130 DLHQIIRSNQBLSEHCQYFMYQLLRGLKYIHSANVLRDLKPSNLLNANCDLKICDFG 189  
QY 183 LARPSSEDMTTEYVTRWTRAPPELLNSTDYSA--DVMSVGCIFMELINRQPLFPGRDH 241  
Db 190 LARPNIEENNTTEYVTRWTRAPPELLNSTDYTAADVMSVGCIFMELMNRKPLFGGKH 249  
QY 242 MHQRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRTFASMPRVPQPAALDLIERM 301  
Db 250 VHQIRLTELGTPTDDELGFIRNEDARKYMRHLPOYPRTFASMPRVPQPAALDLIERM 309  
QY 302 LTFNPLQRIITVEALDHPYLERLHDIADPEPICLEPFSDPEQKALNEDQMQLIFNEAIE 361  
Db 310 LTFDPTRIITVEALDHPYLERLHDIADPEPICLEPFSDPEQKALNEDQMQLIFNEAIE 369  
QY 362 MNP 364  
Db 370 LNP 372

## RESULT 4

US-08-837-593-7  
; Sequence 7, Application US/08837593  
; Patent No. 5977442  
; GENERAL INFORMATION:  
; APPLICANT: Klessig, Daniel F.  
; APPLICANT: Zhang Zhuqun  
; TITLE OF INVENTION: "No. 5977442el Salicylic Acid Induced  
; TITLE OF INVENTION: Map Kinase and its Use for Enhanced Disease Resistance in Plan  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman,  
; ADDRESSEE: P.C.  
; STREET: 1601 Market Street, Suite 720  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: United States of America  
; ZIP: 19103-2307  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/837,593  
; FILING DATE: April 21, 1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/029,805  
; FILING DATE: October 25, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Reed, Janet E.  
; REGISTRATION NUMBER: 36,252  
; REFERENCE/DOCKET NUMBER: Rutgers 97-0016  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 563-4100  
; TELEFAX: (215) 563-4044  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 370 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal

## ORIGINAL SOURCE:

US-08-837-593-7

Query Match 75.3%; Score 1471.5; DB 1; Length 370;  
Best Local Similarity 72.7%; Pred. No. 4e-145;  
Matches 264; Conservative 58; Mismatches 40; Indels 1; Gaps 1;  
QY 3 GAPVAEPRFTMTGGRYLLDYIFGNKFEVTNKKYQRPIMPIGRGAYGIVCSVMNFETREMV 62  
Db 5 GGOYTDFFPAVDTHGGQFISYDIFGSLFEITSKYRPPPIIGRGAYGIVCSVLDTETNELV 64  
QY 63 AIKKIANAFNDMDAKRTLEIKLRLHLDHENIIGIRVDVPPPIPOAFNDVYIATLMDT 122  
Db 65 AMKKIANAFNDMDAKRTLEIKLRLHLDHENIIGIRVDVPPPIPOAFNDVYIATLMDT 124  
QY 123 DLHIIIRSNQBLSEHCQYFLYQILRLGLKYIHSANVIHRDLKPSNLLNANCDLKICDFG 182  
Db 125 DLHQIIRSNQBLSEHCQYFLYQILRLGLKYIHSANVIHRDLKPSNLLNANCDLKICDFG 184  
QY 183 LARPSSEDMTTEYVTRWTRAPPELLNSTDYSA--DVMSVGCIFMELINRQPLFPGRDH 241  
Db 185 LARPTSEDFMTEYVTRWTRAPPELLNSTDYTAADVMSVGCIFMELMNRKPLFGGKH 244  
QY 242 MHQRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRTFASMPRVPQPAALDLIERM 301  
Db 245 VHQIRLTELGTPTDDELGFIRNEDARKYMRHLPOYPRTFASMPRVPQPAALDLIERM 304  
QY 302 LTFNPLQRIITVEALDHPYLERLHDIADPEPICLEPFSDPEQKALNEDQMQLIFNEAIE 361  
Db 305 LTFDPTRIITVEALDHPYLERLHDIADPEPICLEPFSDPEQKALNEDQMQLIFNEAIE 364  
QY 362 MNP 364  
Db 365 LNP 367

## RESULT 5

US-08-837-593-4  
; Sequence 4, Application US/08837593  
; Patent No. 5977442  
; GENERAL INFORMATION:  
; APPLICANT: Klessig, Daniel F.  
; APPLICANT: Zhang Zhuqun  
; TITLE OF INVENTION: "No. 5977442el Salicylic Acid Induced  
; TITLE OF INVENTION: Map Kinase and its Use for Enhanced Disease Resistance in Pla  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman,  
; ADDRESSEE: P.C.  
; STREET: 1601 Market Street, Suite 720  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: United States of America  
; ZIP: 19103-2307  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/837,593  
; FILING DATE: April 21, 1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/029,805  
; FILING DATE: October 25, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Reed, Janet E.  
; REGISTRATION NUMBER: 36,252  
; REFERENCE/DOCKET NUMBER: Rutgers 97-0016  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 563-4100  
; TELEFAX: (215) 563-4044



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;
;
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 387 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-837-593-4

Query Match 74.1%; Score 1448; DB 1; Length 387;
Best Local Similarity 71.6%; Pred. No. 1.2e-142;
Matches 265; Conservative 59; Mismatches 45; Indels 8; Gaps 3;

QY 2 DGAP-----VAFRPTWTHGGRYLLYDIFGNKFEVTKYQPPIMPIGRGAYGIVCSVMN 55
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
15 DAAPAPPQMGIEIPAVLSHGGRFIQYINFGNIFEVTKYKPPIMPIGRGAYGIVCSAHN 74
QY 56 FETREVAIKKIANAFNNDMAKRTLRKILRLHLDHENIIGIRDVIPPPIQAFNDVYI 115
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
75 SETNEHAVAKKIANAFNNDMAKRTLRKILRLHLDHENIIGIRDVIPPPIQAFNDVYI 134
QY 116 ATELMDTDLHHIIRSNQELSEEHCOQFLYQILRGLKYIHSANVHRDLKPSNLLNANCD 175
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
135 AVELMDTDLHIIIRSNQALSEEHCOQFLYQILRGLKYIHSANVHRDLKPSNLLNANCD 194
QY 176 LKICDFGLAPPSDSMTTEVYVTRWRAPPELLNSTDYSAA-DVWSVGCIFMELINRQP 234
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
195 LKICDFGLARVTSETDFMTTEVYVTRWRAPPELLNSTDYTAADVWSVGCIFMELMDRKP 254
QY 235 LPGRDHOMRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPRVPQAA 294
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
255 LPGRDHVQRLUMELIGTPEDDLGFL-ENAKRYIRQLPPYRQSFQKPEFPHVHPEA 313
QY 295 LDILERMLTNPQRITVEALDHPYLERLHDIADPEICLPESFDFEQKALNEDQMQL 354
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
314 IDLVERMLTDFPRKRITVEDALAHPLYLTSLHDSIDPEVCMVTFDFEQHALTEEQMKEL 373
QY 355 IFNEALEMNP 364
Db : : : : :
374 IYREALAFNP 383

RESULT 6
US-08-837-593-3
; Sequence 3, Application US/08837593
; Patent No. 5977442
; GENERAL INFORMATION:
; APPLICANT: Klessig, Daniel P.
; APPLICANT: Zhang Zhuqun
; TITLE OF INVENTION: "No. 5977442el Salicylic Acid Induced
; TITLE OF INVENTION: Map Kinase and its Use for Enhanced Disease Resistance in Plant
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman,
; ADDRESSEE: P.C.
; STREET: 1601 Market Street, Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: United States of America
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,593
; FILING DATE: April 21, 1997
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;
;
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/029,805
; FILING DATE: October 25, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Janet E.
; REGISTRATION NUMBER: 36,252
; REFERENCE/DOCKET NUMBER: Rutgers 97-0016
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-4100
; TELEFAX: (215) 563-4044
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 393 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-837-593-3

Query Match 74.0%; Score 1445.5; DB 1; Length 393;
Best Local Similarity 72.6%; Pred. No. 2.3e-142;
Matches 267; Conservative 52; Mismatches 44; Indels 5; Gaps 3;

QY 5 PVA---EFRPTWTHGGRYLLYDIFGNKFEVTKYQPPIMPIGRGAYGIVCSVMNFTREM 61
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
26 PVAGIDNTPATLSHGGRFIQYINFGNIFEVTKYKPPIMPIGRGAYGIVCSALNSETNEH 85
QY 62 VAIKIANAFNNDMAKRTLRKILRLHLDHENIIGIRDVIPPPIQAFNDVYIATELMD 121
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
86 VAIKIANAFNNDMAKRTLRKILRLHLDHENIIGIRDVIPPPIQAFNDVYIATELMD 145
QY 122 TDLHHIIRSNQELSEEHCOQFLYQILRGLKYIHSANVHRDLKPSNLLNANCDLKICDF 181
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
146 TDLHQIIRSNQALSEEHCOQFLYQILRGLKYIHSANVHRDLKPSNLLNANCDLKICDF 205
QY 182 GLARPSDSMTTEVYVTRWRAPPELLNSTDYSAA-DVWSVGCIFMELINRQPLPGRD 240
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
206 GLARVTSETDFMTTEVYVTRWRAPPELLNSTDYTAADVWSVGCIFMELMDRKPPLPGRD 265
QY 241 HMHOMRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPRVPQAAOLDIER 300
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
266 HVHQRLMELIGTPEAEAEFL-ENAKRYIRQLPPYRQSFVKEKFPVNPAAIDLVEK 324
QY 301 MLTFNPLQRITVEALDHPYLERLHDIADPEICLPESFDFEQKALNEDQMQLIFNEAI 360
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
325 MLTFDPRRITVEDALAHPLYLTSLHDSIDPEVCMVTFDFEQHALTEEQMKELIYREG 384
QY 361 ENMNPRIY 368
Db : : : : :
385 AFNPEYQH 392

RESULT 7
US-08-837-593-2
; Sequence 2, Application US/08837593
; Patent No. 5977442
; GENERAL INFORMATION:
; APPLICANT: Klessig, Daniel P.
; APPLICANT: Zhang Zhuqun
; TITLE OF INVENTION: "No. 5977442el Salicylic Acid Induced
; TITLE OF INVENTION: Map Kinase and its Use for Enhanced Disease Resistance in Plant
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman,
; ADDRESSEE: P.C.
; STREET: 1601 Market Street, Suite 720
; CITY: Philadelphia
```







; PRIOR APPLICATION NUMBER: 60/209,585
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: 09/739,455
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Dictyostelium discoideum
US-10-153-919-23

Query Match 47.2%; Score 921.5; DB 2; Length 304;
Best Local Similarity 59.2%; Pred. NO. 9.1e-88;
Matches 174; Conservative 52; Mismatches 63; Indels 5; Gaps 3;

QY 42 IGRGAYGVCSVMNFTREVMVAIKKIANAFNNDMDAKRTLRLEIKLRLHLDHNIIGIRDV 101
DB 11 IGHGAYGVVCSAKDNLTGKVAIKKISKAFDNLKDKTKRTLRLEHLRHPKHENLISIKDI 70

QY 102 IPPPIQAFNDVYIATLMDTDLHHIIRSNQELSEHCQVFLYQILRLGLKYIHSANVHR 161
DB 71 LKENSKEQEDVYIVSELMDTDLHQIITSQPPLSDHCHQVYVYQMLRGLKXHSANVLR 130

QY 162 DLKPSNLLNANCDLKICDPGLAR--PSSSDMMTEYVVRWYRAPELLLNSTDYS--AAD 218
DB 131 DLKPSNLLINEDCLLKICDGLARVEDATHQGFMTYVATRWYRAPEVILSWNKYTKAID 190

QY 219 VNSVGCIFMELINRQPLFGDRDHQMLRITVEIGTPTDDELGFNEDARKYMR--HLP 276
DB 191 INSVGCIFAEILGRKPLFOGKYHQIHTLIETIGSPSEEDICNIANEQARQPIRSLNMG 250

QY 277 QYPRRTFASMPFRVQPAALDLIERMLTFNPLQRTITVEALDHPYLRRLHLDIADE 330
DB 251 NQPKVFNANFPKAPDAIDLLERMLYFDPKSLITVEEALAHYPFQSLHDPSDE 304

RESULT 15
US-09-417-197-57
; Sequence 57, Application US/09417197
; Patent No. 6518021
; GENERAL INFORMATION:
; APPLICANT: Ole THASTRUP, et al.
; TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An
; FILE REFERENCE: 3759-0110P
; CURRENT APPLICATION NUMBER: US/09/417,197
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 57
; LENGTH: 624
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mERK1-F64L-S65T-GFP fusion
US-09-417-197-57

Query Match 46.3%; Score 904; DB 2; Length 624;
Best Local Similarity 50.9%; Pred. NO. 1.8e-85;
Matches 175; Conservative 65; Mismatches 96; Indels 8; Gaps 5;

QY 26 GNKFVETNKQPPIMPIRGAYGVCSVMNFTREVMVAIKKIANAFNNDMDAKRTLRLEIK 85
DB 34 GQPFVGVPRY-TQLQYIGEGAYGVSSAYDVRKTRVAIKKI-SPFEHQTYCQRTLRLEIQ 91

QY 86 LLRHLDHENTIGIRDVTPPIQAFNDVYIATLMDTDLHHIIRSNQELSEHCQVFLYQ 145
DB 92 ILLRFRHENVIGIRDILRAPTRLEAMRDVYIVQDLMETDLYKLLKS-QQLSNDHICYFLYQ 150

QY 146 ILRGLKYIHSANVHRDLKPSNLLNANCDLKICDGLAR----PSSSDMMTEYVVRW 201
DB 151 ILRGLKYIHSANVLRDLKPSNLLNTTCDLKICDGLARIADPEHDHTGFLTYYVATRW 210

QY 202 YRAPELLLNSTDYS--AADVNSVGCIFMELINRQPLFGDRDHQMLRITVEIGTPTDDEL 260
DB 211 YRAPEIMLNSKGYTKSIDWSVGCILAEMLSNRPIFGKHVLDQLNHLILGILGSPSQEDL 270

QY 261 GFIRNEDARKYMRHLPOYPRTFASMPFRVQPAALDLIERMLTFNPLQRTITVEALDHPY 320
DB 271 NCIIINMKARNYLQSLPSKTKVAAKLFPKSDSKALDLDRLMTFNPKNKRITVEEALAHYPY 330

QY 321 LERLHLDIADEPICLEPPFSDFEQKALNEDQMKQLIFNEAIEHNP 364
DB 331 LEQYDPTDEPVAEEPTFDMELDDLPKERLXELIFQETARQP 374

Search completed: December 27, 2005, 20:42:00
Job time : 47 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 27, 2005, 20:30:11 ; Search time 39 Seconds  
(without alignments)  
907.892 Million cell updates/sec

Title: US-10-768-886-2  
Perfect score: 1953  
Sequence: 1 MDGAPVAEPRPTWTHGGRYL.....DQMKQLIFNEAIEIMPNIY 368

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1819.5	93.2	369	2 S56638	mitogen-activated
2	1504.5	77.0	371	2 T09622	protein kinase MMK
3	1472.5	75.4	370	2 T47504	mitogen-activated
4	1472.5	75.4	375	2 T03971	mitogen-activated
5	1471.5	75.3	370	2 S40469	mitogen-activated
6	1448	74.1	387	2 S48123	mitogen-activated
7	1445.5	74.0	393	2 S51321	mitogen-activated
8	1442	73.8	395	2 S40472	mitogen-activated
9	1441.5	73.8	371	2 T14915	mitogen-activated
10	1437	73.6	394	2 S33635	mitogen-activated
11	1327.5	68.0	371	2 S51320	mitogen-activated
12	1325.5	67.9	371	2 S60121	mitogen-activated
13	1315.5	67.4	376	2 S40470	mitogen-activated
14	1277.5	65.4	369	2 C86146	hypothetical prote
15	1257.5	64.4	376	2 S40471	mitogen-activated
16	1244.5	63.7	363	2 C86214	hypothetical prote
17	1230	63.0	373	2 T13024	probable protein k
18	1229	62.9	393	2 T47803	mitogen-activated
19	1210.5	62.0	406	2 D84898	probable mitogen-a
20	1031	52.8	372	2 S39559	mitogen-activated
21	1024	52.4	415	2 A56042	mitogen-activated
22	1017	52.1	384	2 S52989	mitogen-activated,
23	981	50.2	370	2 F86236	protein F14N23.9 [
24	979	50.1	368	2 B84561	MAP kinase (ATMPK7
25	972	49.8	368	2 S40473	mitogen-activated
26	966	49.5	376	2 F96619	protein T30E16.13
27	940	48.1	361	2 C85430	MAP kinase like pr
28	923.5	47.3	356	2 T51944	pathogenicity MAP
29	906	46.4	361	2 T51943	mitogen-activated

30	904	46.3	377	2 S28184	Ca2+/calmodulin-de
31	902	46.2	380	2 JC1451	Ca2+/calmodulin-de
32	902	46.2	392	2 JW0052	extracellular sign
33	901	46.1	369	2 A60041	Ca2+/calmodulin-de
34	898	46.0	376	2 A36978	MAP kinase mpk-1 (
35	898	46.0	444	2 A36977	MAP kinase sur-1 (
36	897	45.9	372	2 S15663	protein kinase (EC
37	894	45.8	353	2 S28548	protein kinase (EC
38	887	45.4	379	1 A48082	MAP kinase 3 (EC 2
39	878	45.0	360	1 JQ1400	MAP kinase 1 (EC 2
40	877	44.9	358	2 S16444	mitogen-activated
41	877	44.9	358	2 A40033	protein kinase (EC
42	877	44.9	360	2 S25011	protein kinase (EC
43	877	44.9	369	2 JW0053	extracellular sign
44	862	44.1	361	2 A39754	mitogen-activated
45	855.5	43.8	362	2 A47211	protein kinase ERK

ALIGNMENTS

RESULT 1

S56638  
mitogen-activated protein kinase 1 homolog (clone AspK9) - oat  
N;Alternate names: MAP1 kinase  
C;Species: Avena sativa (oat)  
C;Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 09-Jul-2004  
C;Accession: S56638  
R;Huttly, A.K.; Phillips, A.L.  
Plant Mol. Biol. 27, 1043-1052, 1995  
A;Title: Gibberellin-regulated expression in oat aleurone cells of two kinases that sho  
A;Reference number: S56638; MUID:95284341; PMID:7766874  
A;Accession: S56638  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-369 <HUT>  
A;Cross-references: UNIPROT:Q43379; UNIPARC:UPI00000AA427; EMBL:X79993; NID:9871983; PI  
C;Superfamily: Kinase-related transforming protein; protein kinase homology  
C;Keywords: ATP; phosphotransferase; protein kinase  
F;33-322/Domain: protein kinase homology <KIN>  
F;42-50/Region: protein kinase ATP-binding motif

Query Match	93.2%;	Score	1819.5;	DB 2;	Length	369;	
Best Local Similarity	91.3%;	Pred. No.	7.3e-69;				
Matches	337;	Conservative	20;	Mismatches	11;	Gaps	1;
Qy	1	MDGAPVAEPRPTWTHGGRYLLYDIFGNKEVTNKYQPPIMPPIGRGAYGIVCSVMNPFRE	60				
Db	1	MDGAPVAEPRPTWTHGGRYLLYDIFGNKEVTNKYQPPIMPPIGRGAYGIVCSVMNPFRE	60				
Qy	61	MVAIKKIANA FNNDDAKRTLRKILRLHLDHENIIGIRDVIPPPIPOAFNDVVIATELM	120				
Db	61	MVAIKKIANA FNNDDAKRTLRKILRLHLDHENIIGIRDVIPPPIPOAFNDVVIATELM	120				
Qy	121	DTDLHHIIRSNQSLSEHCOFYQLRGLKYTHSANVIHRDLKPSNLLNANCDLKICD	180				
Db	121	DTDLHHIIRSNQSLSEHCOFYQLRGLKYTHSANVIHRDLKPSNLLNANCDLKICD	180				
Qy	181	FGLARPSSESDMMTEVVTWYRAPPELLNSTDYSAADVWSVGCIFMELINRQPLPFR	239				
Db	181	FGLARPSSESDMMTEVVTWYRAPPELLNSTDYSAADVWSVGCIFMELINRQPLPFR	240				
Qy	240	DHMHQRLITEVIGTPTDDELGFIRNEDARKYRHLPOYPRRTFASMPFRVQPAALDLIE	299				
Db	241	DHMHQRLITEVIGTPTDDELGFIRNEDARKYRHLPOYPRRTFASMPFRVQPAALDLIE	300				
Qy	300	RMLTFNPLOQRITVEBALDHPYLERLHDIADPEICLPFPSPDFEQKALNEQMKQLIFNEA	359				
Db	301	RMLTFNPLOQRITVEBALDHPYLERLHDIADPEICLPFPSPDFEQKALNEQMKQLIFNEA	360				
Qy	360	IENPNIRY 368					
Db	361	LELNPNIY 369					

```
RESULT 2
T09622
protein kinase WMK4 (EC 2.7.1.-), cold- and drought-induced - alfalfa
C:Species: Medicago sativa (alfalfa)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T09622
R:Jonak, C.; Kiegerl, S.; Lighter, W.; Barker, P.; Huskisson, N.; Hirt, H.
Proc. Natl. Acad. Sci. U.S.A. 93, 11274-11279, 1996
A:Title: Signaling in plants: a mitogen-activated protein kinase pathway is activated by
A:Reference number: Z16782; MUID:97008170; PMID:8855346
A:Accession: T09622
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-371 <JON>
A:Cross-references: UNIPROT:Q24077; UNIPARC:UPI00000A8D84; EMBL:X82270; NID:g1667372; PI
C:Genetics:
A:Gene: WMK4
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: phosphotransferase; protein kinase
F:36-325/Domain: protein kinase homology <KIN>

Query Match 77.0%; Score 1504.5; DB 2; Length 371;
Best Local Similarity 74.4%; Pred. No. 7e-56;
Matches 268; Conservative 56; Mismatches 35; Indels 1; Gaps 1;

QY 6 VAEFRPTMTGGGRYLLYDIFGNKFEVTNKKYQPIPIGKRGAYGIVCSVMNFETREVMV 65
DB 9 VAEFPVAVQTHGGQGVQVNFNDVETAKTRPPIPIGKRGAYGIVCSLNTETNELVAVK 68
QY 66 KIANAFNNDMDAKRTLREIKLRLHLDHENIIGIRDVIPPPIPOAFNDVVIATIELMDTLH 125
DB 69 KIANAFNNDMDAKRTLREIKLRLHLDHENVIGLRDVIPLRLREFNDVVIATIELMDTLH 128
QY 126 HIIRSNQELSEHCQYFLYLGLKLYIHSANVIHRDLKPSNLLNANCDLKICDPGLAR 185
DB 129 QIIRSNQELSEHCQYFLYLGLKLYIHSANVIHRDLKPSNLLNANCDLKICDPGLAR 188
QY 186 PSESDDMTTEYVTVRWYRAPELLNSTDY-SAADVMSVGCIFMELINRQPLPFGGRDHQ 244
DB 189 PTMESDFMTEYVTVRWYRAPELLNSTDYSAIDVMSVGCIFMELNNKPLPFGKDHQ 248
QY 245 MRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYRRTFASMPFRVQPAALDLIERMLTF 304
DB 249 MRLITELLGPTDADVLKNDARRYIRQLPOYRQPLNRVPPHVLPLAIDLVDKMLTI 308
QY 305 NPLQRTVTEALDHPYLERLHDIADSPICLPEPSPDFEQKALNEDQMOLIFNEAIEIMP 364
DB 309 DPTRRITVTEALAHPLYLEKLDVADBPICWEPSPDFEQQLHDEEQIKEMIYREALALNP 368

RESULT 3
T47504
mitogen-activated protein kinase 3 - Arabidopsis thaliana
N:Alternate names: protein F9K21.220
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T47504
R:Jordan, N.; Bangert, S.; Widelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Lemcke, K.
submitted to the Protein Sequence Database, February 2000
A:Reference number: Z24467
A:Accession: T47504
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-370 <JON>
A:Cross-references: UNIPROT:Q39023; UNIPARC:UPI0000001AE1; EMBL:AL138657
A:Experimental source: cultivar Columbia; BAC clone F9K21
C:Genetics:
A:Map position: 3
A:Intron: 53/2; 96/3; 142/3; 253/3; 315/1
A>Note: F9K21.220
C:Superfamily: Kinase-related transforming protein; protein kinase homology
```

```
Query Match 75.4%; Score 1472.5; DB 2; Length 370;
Best Local Similarity 72.7%; Pred. No. 1.5e-54;
Matches 264; Conservative 58; Mismatches 40; Indels 1; Gaps 1;

QY 3 GAPVAEFPRTMTGGGRYLLYDIFGNKFEVTNKKYQPIPIGKRGAYGIVCSVMNFETREMV 62
DB 5 GGOYTFDPAVETHGGQGVQVNFNDVETAKTRPPIPIGKRGAYGIVCSVLDTETNELV 64
QY 63 AIKTIANAFNNDMDAKRTLREIKLRLHLDHENIIGIRDVIPPPIPOAFNDVVIATIELMDT 122
DB 65 AMKTIANAFNNDMDAKRTLREIKLRLHLDHENIIRDVVPPPLRQSDVVIATIELMDT 124
QY 123 DLHIIIRSNQELSEHCQYFLYLGLKLYIHSANVIHRDLKPSNLLNANCDLKICDPG 182
DB 125 DLHIIIRSNQELSEHCQYFLYLGLKLYIHSANVIHRDLKPSNLLNANCDLKICDPG 184
QY 183 LARPSSEDDMTTEYVTVRWYRAPELLNSTDYSA-DVMSVGCIFMELINRQPLPFGGRDH 241
DB 185 LARPTSENDPMTEYVTVRWYRAPELLNSTDYTAIDVMSVGCIFMELNNKPLPFGKDH 244
QY 242 MHQMLITEVIGTPTDDELGFIRNEDARKYMRHLPOYRRTFASMPFRVQPAALDLIERM 301
DB 245 VHQMELLTELLGPTDESGLGFTHNEDAKRYIRQLPNFPROPLAKULFSHVNPMAIDLVDK 304
QY 302 LTFNPLQRTVTEALDHPYLERLHDIADSPICLPEPSPDFEQKALNEDQMOLIFNEATE 361
DB 305 LTFDPPNRITVQALNHQYLAKLHDPNDEPICQEPSPDFEQQLDEEQIKEMIYQEAIA 364
QY 362 WNP 364
DB 365 LNP 367

RESULT 4
T03971
mitogen-activated protein kinase (EC 2.7.1.-) WIPK - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T03971
R:Seo, S.; Okamoto, M.; Seto, H.; Ishizuka, K.; Sano, H.; Ohashi, Y.
Science 270, 1988-1992, 1995
A:Title: Tobacco MAP kinase: a possible mediator in wound signal transduction pathways.
A:Reference number: Z15170; MUID:96123271; PMID:8533090
A:Accession: T03971
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-375 <SEO>
A:Cross-references: UNIPROT:Q40598; UNIPARC:UPI00000A4PF8; EMBL:D61377; NID:g1136297; P;
C:Comment: MAP kinase is part of the initial response of higher plants to mechanical wou
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; phosphotransferase
F:40-329/Domain: protein kinase homology <KIN>

Query Match 75.4%; Score 1472.5; DB 2; Length 375;
Best Local Similarity 72.5%; Pred. No. 1.5e-54;
Matches 263; Conservative 58; Mismatches 41; Indels 1; Gaps 1;

QY 3 GAPVAEFPRTMTGGGRYLLYDIFGNKFEVTNKKYQPIPIGKRGAYGIVCSVMNFETREMV 62
DB 10 GGOYTFDPAVETHGGQGVQVNFNDVETAKTRPPIPIGKRGAYGIVCSVLNTSELNV 69
QY 63 AIKTIANAFNNDMDAKRTLREIKLRLHLDHENIIGIRDVIPPPIPOAFNDVVIATIELMDT 122
DB 70 AVKTIANAFNNDMDAKRTLREIKLRLHLDHENVIGLRDVIPLRLREFSDVVIATIELMDT 129
QY 123 DLHIIIRSNQELSEHCQYFLYLGLKLYIHSANVIHRDLKPSNLLNANCDLKICDPG 182
DB 130 DLHIIIRSNQELSEHCQYFMYQLLGLKLYIHSANVLHRLKPSNLLNANCDLKICDPG 189
QY 183 LARPSSEDDMTTEYVTVRWYRAPELLNSTDYSA-DVMSVGCIFMELINRQPLPFGGRDH 241
DB 190 LARPNIENNTTEYVTVRWYRAPELLNSTDYTAIDVMSVGCIFMELNNKPLPFGKDH 249
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A;Cross-references: UNIPROT:Q40532; UNIPARC:UPI00000130582; EMBL:X63880; NID:G634069; PID: C;Genetics:

A;Gene: ntcf4

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

P;57-345/Domain: protein kinase homology <KIN>

P;66-74/Region: protein kinase ATP-binding motif

Query Match 74.0%; Score 1445.5; DB 2; Length 393;  
Best Local Similarity 72.6%; Pred. No. 2e-53;  
Matches 267; Conservative 52; Mismatches 44; Indels 5; Gaps 3;

QY 5 PVA---EPRTWTHGGRYLLDYIFGNKFEVTKYQPPIMPGRGAYGVCSVWVFTRM 61  
DB 26 PVAGIDNIPATLSHGGRFIQYNIFGNIFEVTAKYKPPIMPGRGAYGVCSALNSETH 85  
QY 62 VAIKKIANAFNDMDAKRTLRKLRHLDHENIGIRDVIPPPIQAFNDVYIATLMD 121  
DB 86 VALKIANAFDNKIDAKRTLRKLRHLDHENIVAIRDIIPPPQREAFNDVYIATLMD 145  
QY 122 TDLHIIIRSNQELSEHCQVFLYQILRGLKYIHSANVHRDLKPSNLLNANCDLKICDF 181  
DB 146 TDLHQIIRSNQELSEHCQVFLYQILRGLKYIHSANVHRDLKPSNLLNANCDLKICDF 205  
QY 182 GLARPSSEDMTEYVVTWYRAPELLLNSTDYSAA-DWVSVCIFMELINRQPLPPGRD 240  
DB 206 GLARVTSDFMTEYVVTWYRAPELLLNSTDYSAA-DWVSVCIFMELMDRKLPPGRD 265  
QY 241 HHOMBLITEVIGTPTDDELGFTRNEDARKYMHLPQYPRRTFASMPVQPAALDLIER 300  
DB 266 HHQLRLMELIGTPEAEFNL-NEAKRYIKQLPPYRQSFVEFPHVNPAAIDLVK 324  
QY 301 MLTFNPLQRIITVEALDHPYLERLHDADEPICLEPFSEDFEQKALNEDQMQLIFNEAI 360  
DB 325 MLTFDPRRITVEDALAHPLYLTLSDISDEPVCMTFFNDFEQHALTEQMKELIYREGI 384  
QY 361 EKNPNTRY 368  
DB 385 AFNPEYQH 392

RESULT 8

S40472

micogen-activated protein kinase 6 (EC 2.7.1.1) - Arabidopsis thaliana

N;Alternate names: MAP kinase (ATMPK6)

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 06-Oct-1994 #sequence\_revision 19-Jan-1996 #text\_change 09-Jul-2004

R;Accession: S40472; E84870

R;Mizoguchi, T.; Hayashida, N.; Yamaguchi-Shinozaki, K.; Kamada, H.; Shinozaki, K. FEBS Lett. 336, 440-444, 1993

A;Title: ATMPK6: a gene family of plant MAP kinases in Arabidopsis thaliana.

A;Reference number: S40469; MUID:94109583; PMID:8282107

A;Accession: S40472

A;Molecule type: mRNA

A;Residues: 1-395 <MIZ>

A;Cross-references: UNIPROT:Q39026; UNIPARC:UPI00000014BF; EMBL:D21842; NID:G457403; PID: R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: E84870

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-395 <STO>

A;Cross-references: UNIPARC:UPI00000014BF; GB:AE002093; NID:G2281091; PIDN:AAB64027.1; C;Genetics:

A;Gene: MPK6; At2g43790

A;Map position: 2

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

P;60-348/Domain: protein kinase homology <KIN>

F;69-77/Region: protein kinase ATP-binding motif

Query Match 73.8%; Score 1442; DB 2; Length 395;  
Best Local Similarity 72.4%; Pred. No. 2.8e-53;  
Matches 270; Conservative 46; Mismatches 45; Indels 12; Gaps 3;

QY 3 GAPVAEFRP-----TWTHGGRYLLDYIFGNKFEVTKYQPPIMPGRGAYGVCS 52  
DB 20 GFPAAPSPQMBGIENIPATLSHGGRFIQYNIFGNIFEVTAKYKPPIMPGRGAYGVCS 79  
QY 53 VVNPETREWVAIKKIANAFNDMDAKRTLRKLRHLDHENIGIRDVIPPPIQAFND 112  
DB 80 ANNSTNSVALKIANAFDNKIDAKRTLRKLRHLDHENIVAIRDIIPPLRNAFND 139  
QY 113 VYIATLMDTDLHIIIRSNQELSEHCQVFLYQILRGLKYIHSANVHRDLKPSNLLNA 172  
DB 140 VYIATLMDTDLHIIIRSNQELSEHCQVFLYQILRGLKYIHSANVHRDLKPSNLLNA 199  
QY 173 NCDLKICDFGLARPSSEDMTEYVVTWYRAPELLLNSTDYSAA-DWVSVCIFMELIN 231  
DB 200 NCDLKICDFGLARVTSDFMTEYVVTWYRAPELLLNSTDYSAAIDVMSVGCIFMELMD 259  
QY 232 RQPLPPGRDHOMBLITEVIGTPTDDELGFTRNEDARKYMHLPQYPRRTFASMPVQ 291  
DB 260 RKPLPPGRDHVHQLRLMELIGTPEAEFNL-NEAKRYIKQLPPYRQSFITDKPPTVH 318  
QY 292 PAALDLIERMUTFNPLQRIITVEALDHPYLERLHDADEPICLEPFSEDFEQKALNEDQM 351  
DB 319 PLAIDLEKMLTDFPRRITVLDALAHPLYLTLSDISDEPCTIPFNFDFENHALSEQM 378  
QY 352 KQLIFNEAIENP 364  
DB 379 KELIYREALAFNP 391

RESULT 9

Ti4915

mitogen-activated protein kinase I (EC 2.7.1.1) - parsley

N;Alternate names: MAP kinase I

C;Species: Petroselinum crispum (parsley)

C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004

C;Accession: Ti4915

R;Rigterink, W.; Kroj, T.; zur Nieden, U.; Hirt, H.; Scheel, D. Science 276, 2054-2057, 1997

A;Title: Receptor-mediated activation of a MAP kinase in pathogen defense of plants.

A;Reference number: Z18265; MUID:97342856; PMID:9197271

A;Accession: Ti4915

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-371 <LIIG>

A;Cross-references: UNIPROT:O04694; UNIPARC:UPI00000A9255; EMBL:Y12785; NID:G2231033; PID: C;Comment: MAP kinase is part of the initial response of higher plants to mechanical wounding

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Keywords: ATP; phosphotransferase

F;36-325/Domain: protein kinase homology <KIN>

Query Match 73.8%; Score 1441.5; DB 2; Length 371;  
Best Local Similarity 72.1%; Pred. No. 2.8e-53;  
Matches 259; Conservative 56; Mismatches 43; Indels 1; Gaps 1;

QY 8 EPRPTWTHGGRYLLDYIFGNKFEVTKYQPPIMPGRGAYGVCSVMPETREWVAIKKI 67  
DB 11 DFPALQTHGGGFQIYNIFGNLFQVTKYRPPIMPGRGAYGVCSIMNTETNEMVAVKKI 70  
QY 68 ANAFNDMDAKRTLRKLRHLDHENIGIRDVIPPPIQAFNDVYIATLMDTDLHII 127  
DB 71 ANAFONYMDAKRTLRKLRHLDHENIVAIRDIIPPLRRREFTDVYIATLMDTDLHQI 130  
QY 128 IRSNQLSEHCQVFLYQILRGLKYIHSANVHRDLKPSNLLNANCDLKICDFGLARPS 187  
DB 131 IRSNQLSEHCQVFLYQILRGLKYIHSANVHRDLKPSNLLNANCDLKICDFGLAREN 190  
QY 188 SESDMTEYVVTWYRAPELLLNSTDYSAA-DWVSVCIFMELINRQPLPPGRDHQHWQR 246



Db	11	RGVPTHGGRYLQYNIYGNLFEVSRKYVPIRSVGRGAGYICAAVNAATREBEVAIKKIGN	70
Qy	70	AFNNDMDAKRTLEIKLRHLDHENIIGIRDVIPPPIQAFNDVYIATELMDTDLHHIIR	129
Db	71	AFDNRIDAKRTLEIKLRHMDHENVMSIKDIIRPQKENFHVYIVSELMDTDLHQIIR	130
Qy	130	SNQELSEBHCQFLYQIIRGLKYIHSANVHRDLKPSNLLNANCDLKI CD FGLARPSSE	189
Db	131	SNQPMTDHCRYFVYQLLRGLKYHSANVLRDLKPSNLLNANCDLKI GDFGLARTTSE	190
Qy	190	SDMTTEYVWYRPAPELLNSTDYSAADVWSVGCIFMELINRQPLPGRDHMHQWELI	248
Db	191	TDFTMYVWYRPAPELLNCSEYTAIDAIDWSVGCILGEIVTRQPLPGRDYVHQLRIV	250
Qy	249	TEVIGTDDDELGFIRNEDARKYMRHLPOYPRRTFASMFPRVQPAALDLIERMLTTFNPLQ	308
Db	251	TELGSPDDASIGPLRSNARYVRLPOYPKQNFSAFPNMSGAVDLLEKMLIFDPSK	310
Qy	309	RITVEALDHPYLERLHDIADBPICLBPSPDFEQKALNEQDKOLIFNEAIEWNP	365
Db	311	RKVDEALCHPYMAPLHDINEBPVCARPSDFEPFETEDIKELIWKESVRFNPD	367
RESULT 13			
S40470			
mitogen-activated protein kinase 4 (EC 2.7.1.-) - Arabidopsis thaliana			
N;Alternate names: MAP kinase			
C;Species: Arabidopsis thaliana (mouse-ear cress)			
C;Date: 06-Oct-1994 #sequence revision 19-Jan-1996 #text_change 09-Jul-2004			
C;Accession: S40470, T01707, H85017			
R;Mitoguchii, T.; Hayaashida, N.; Yamaguchi-Shinozaki, K.; Kamada, H.; Shinozaki, K.			
FEBS Lett. 336, 440-444, 1993			
A;Title: ATPKs: a gene family of plant MAP kinases in Arabidopsis thaliana.			
A;Reference number: S40469, MUID:94109583; PMID:8282107			
A;Accession: S40470			
A;Molecule type: mRNA			
A;Residues: 1-376 <M2>			
A;Cross-references: UNIPROT:Q39024; UNIPARC:UPI000016DA9D; EMBL:D21840; NID:g457399; PID			
R;Scheet, P.; Maggi, L.			
submitted to the EMBL Data Library, June 1997			
A;Description: The sequence of A. thaliana IG002N01.			
A;Reference number: Z14407			
A;Accession: T01707			
A;Status: preliminary; translated from GB/EMBL/DBJ			
A;Molecule type: DNA			
A;Residues: 1-40,'N',59-147,153-312,'D',314-376 <SCH>			
A;Cross-references: UNIPARC:UPI000016DA7B; EMBL:AF007269; NID:g2191126; PIDN:AB61033,1;			
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring			
Nature 402, 769-777, 1999			
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.			
A;Reference number: A85001; MUID:20083488; PMID:10617198			
A;Accession: H85017			
A;Status: preliminary			
A;Molecule type: DNA			
A;Residues: 1-312,'D',314-376 <STO>			
A;Cross-references: UNIPARC:UPI000000144E; GB:NC_001268; NID:g7267634; PIDN:CAB80946,1;			
C;Genetics:			
A;Gene: MPK4; AT4G01370			
A;Map position: 4			
A;Introns: 41/2, 101/3; 147/3; 258/3; 320/1			
C;Superfamily: kinase-related transforming protein; protein kinase homology			
F;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase			
F;40-329/Domain: protein kinase homology <KIN>			
F;49-57/Region: protein kinase ATP-binding motif			
Query Match 67.4%; Score 1315.5; DB 2; Length 376;			
Best Local Similarity 66.2%; Pred. No. 4.4e-48;			
Matches 233; Conservative 62; Mismatches 58; Indels 1; Gaps 1;			
Qy	14	THGGRYLLYDFGNKFEVTNKYQPIIMPGRGAGYGVCSVMNFTREMVAIKKIANFNN	73
Db	21	THGSGYQVYVGNLFEVSRKYVPLRIFGRGAGYGVCAATNSGTGEVAIKKIGNAFDN	80

Qy	74	DMDAKRTLEIKLRHLDHENIIGIRDVIPPPIQAFNDVYIATELMDTDLHHIIRSNQE	133
Db	81	IIDAKRTLEIKLRHMDHENVIAVDKIIKPPQRENFNVDVYVELMDTDLHQIRSNQP	140
Qy	134	LSEBHCQFLYQIIRGLKYIHSANVHRDLKPSNLLNANCDLKI CD FGLARPSSEDM	193
Db	141	LTDDHCFRFFYQLLRGLKYHSANVLRDLKPSNLLNANCDLKI GDFGLARTKSETDFM	200
Qy	194	TEYVWYRPAPELLNSTDYSAADVWSVGCIFMELINRQPLPGRDHMHQWELI TEVI	252
Db	201	TEYVWYRPAPELLNCSEYTAIDAIDWSVGCILGEIVTRQPLPGRDYVHQLRILTELI	260
Qy	253	GTPTDDDELGFIRNEDARKYMRHLPOYPRRTFASMFPRVQPAALDLIERMLTTFNPLQRTV	312
Db	261	GSPDSSILGFLRSNARYVRLPOYPRQNFARFPNMSGAVDLLEKMLVFEPSSRTIV	320
Qy	313	EEALDHPYLERLHDIADBPICLBPSPDFEQKALNEQDKOLIFNEAIEWNP	364
Db	321	DEALCHPYLAPLHDINEBPVCVRPNFDFEQPTLTEENIKELIYRETVKFNP	372
RESULT 14			
C86146			
hypochemical protein F22I4.10 [imported] - Arabidopsis thaliana			
C;Species: Arabidopsis thaliana (mouse-ear cress)			
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004			
C;Accession: C86146			
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federapfel, N.A.; Kaul, S.; White, O.; Alonso,			
ansen, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;			
Nature 408, 816-820, 2000			
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;			
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,			
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.			
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,			
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.			
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.			
A;Reference number: A86141; MUID:21016719; PMID:11130712			
A;Accession: C86146			
A;Status: preliminary			
A;Molecule type: DNA			
A;Residues: 1-369 <STO>			
A;Cross-references: UNIPROT:Q9LMM5; UNIPARC:UPI00000A68BA; GB:AB005172; NID:g8920592; PI			
C;Genetics:			
A;Map position: 1			
C;Superfamily: kinase-related transforming protein; protein kinase homology			
Query Match 65.4%; Score 1277.5; DB 2; Length 369;			
Best Local Similarity 64.6%; Pred. No. 1.16e-46;			
Matches 230; Conservative 64; Mismatches 61; Indels 1; Gaps 1;			
Qy	10	RPTWTHGGRYLLYDFGNKFEVTNKYQPIIMPGRGAGYGVCSVMNFTREMVAIKKIAN	69
Db	14	RGVINGRIVQVNVYVGNLFEVSKYVPLRIPGRGASGIVCAAWNSGTGEVAIKKIGN	73
Qy	70	AFNNDMDAKRTLEIKLRHLDHENIIGIRDVIPPPIQAFNDVYIATELMDTDLHHIIR	129
Db	74	AFGNIIDAKRTLEIKLRHMDHNVIAIDIRPPQDNFNDVHIVVELMDTDLHHIIR	133
Qy	130	SNQELSEHCQFLYQIIRGLKYIHSANVHRDLKPSNLLNANCDLKI CD FGLARPSSE	189
Db	134	SNQPLTDHDSRFFLYQLLRGLKYHSANVLRDLKPSNLLNANCDLKI GDFGLARTKSE	193
Qy	190	SDMTTEYVWYRPAPELLNSTDYSAADVWSVGCIFMELINRQPLPGRDHMHQWELI	248
Db	194	TDFTMYVWYRPAPELLNCSEYTAIDAIDWSVGCILGEIVTRQPLPGRDYVHQLRIL	253
Qy	249	TEVIGTDDDELGFIRNEDARKYMRHLPOYPRRTFASMFPRVQPAALDLIERMLTTFNPLQ	308
Db	254	TELGSPDDSSILGFLRSNARYVRLPOYPRQNFARFPNMSGAVDLLEKMLVFDPNR	313
Qy	309	RITVEALDHPYLERLHDIADBPICLBPSPDFEQKALNEQDKOLIFNEAIEWNP	364

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||||:||||| ||| ||: ||: ||: || ||||| :| ||: ||: ||: ||: ||: ||
Db 314 RITVDEALCHPYLAPLHEYNREPVCVRPFHDFEQPSLSTEENIKELIYRESVKFNP 369

RESULT 15
S40471
mitogen-activated protein kinase 5 (EC 2.7.1.1) - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 07-Sep-1994 #sequence_revision 19-Jan-1996 #text_change 09-Jul-2004
C;Accession: S40471
R;Mizoguchi, T.; Hayashida, N.; Yamaguchi-Shinozaki, K.; Kamada, H.; Shinozaki, K.
FEBS Lett. 336, 440-444, 1993
A;Title: ATPKs: a gene family of plant MAP kinases in Arabidopsis thaliana.
A;Reference number: S40469; MUID:94109583; PMID:8282107
A;Accession: S40471
A;Molecule type: mRNA
A;Residues: 1-376 <MIZ>
A;Cross-references: UNIPROT:Q39025; UNIPARC:UPI000016DA9E; EMBL:D21841; NID:9457401; PIR
C;Genetics:
A;Gene: MPK5
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;40-298/Domain: protein kinase homology <KIN>
F;49-57/Region: protein kinase ATP-binding motif

Query Match 64.4%; Score 1257.5; DB 2; Length 376;
Best Local Similarity 63.7%; Pred. No. 1.1e-45;
Matches 225; Conservative 66; Mismatches 61; Indels 1; Gaps 1;

Qy 13 MTHGGRYLLYDIIGNKEEVNKKYQPIPIGRGAYGIVCSVMNFETREMYAIKKIANAFN 72
Db 20 LVHGGRYFYQNVYGNLFVSNKYVPIRPIGRGAYGVCVADVSETHETAIKKIGKAFD 79
Qy 73 NMDAKRTLRKIKLRLHLDHENIIGIRDVIPPPIQAFNDVYIATLMDTDLHHIIRSNQ 132
Db 80 NKVDKRTLRKIKLRLHLENVNVKDIIRPKKEDFDVYIVFELMDTDLHQIIRSNQ 139
Qy 133 ELSEHCQYLYQILRGLKTIHSANVIRDLKPSNLLNANCDLKICDFGLARPSSESDM 192
Db 140 SLNDDHCQYLYQILRGLKTIHSANVIRDLKPSNLLNANCDLKITDFGLARTTSETEY 199
Qy 193 MTEVVTWYTRAPPELLNSTDY-SAADVWSVGCIFMELINRQPLFPGRDHMQRLITEV 251
Db 200 MTEVVTWYTRAPPELLNSSEYTSADVWSVGCIFAFIMTREPFPKGKYYVHQKLITEL 259
Qy 252 IGTPTDDELGIARNEDARKYMRHLPOYPRRTFASMPFRVQPAALDLIERMLTFNPLQRI 311
Db 260 IGSFDGNSLEFLSANGGKVKELPKFPRQNFSAFPFSMNSTADLLEKMLVDFPVKRI 319
Qy 312 VREALDHPYLERLHDIADEPICLEPFSDFEQKALNEDOMKQIFNEAIEMNP 364
Db 320 VREALCPYLSALHDLNDEPVCNSNHFSGFHFEDPSPSTEEIKELVWLESVKFNP 372

Search completed: December 27, 2005, 20:41:08
Job time : 41 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2005, 20:20:31 ; Search time 188 Seconds  
(without alignments)  
860.061 Million cell updates/sec

Title: US-10-768-886-2  
Perfect score: 1953  
Sequence: 1 MDGAPVAEPRPTWTHGGRYL.....DOMKQLIFNEALEMPNIRY 368

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: Genesecp1990s:\*  
3: Genesecp2000s:\*  
4: Genesecp2001s:\*  
5: Genesecp2002s:\*  
6: Genesecp2003as:\*  
7: Genesecp2003bs:\*  
8: Genesecp2004s:\*  
9: Genesecp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1953	100.0	368	8	ADT02330 Rice mito
2	1803.5	92.3	374	3	AAG34157 Zea mays
3	1798.5	92.1	374	4	AAB48046 Signal tr
4	1632.5	83.6	330	3	AAG34158 Zea mays
5	1557.5	79.7	316	3	AAG34159 Zea mays
6	1472.5	75.4	375	2	AAW15512 MAP kinase
7	1448.5	74.2	398	4	AAB48048 Signal tr
8	1442	73.8	382	3	AAG31654 Arabidops
9	1442	73.8	395	3	AAG31653 Arabidops
10	1441	73.8	366	3	AAG31655 Arabidops
11	1438.5	73.7	393	2	AAW61252 Salicylic
12	1423	72.9	398	4	AAB48047 Signal tr
13	1380.5	70.7	423	2	AAW15513 MAP kinase
14	1340.5	68.6	318	8	ADT02332 Plant ful
15	1334.5	68.3	266	8	ADT02332 Rice mito
16	1331.5	68.2	403	8	ADY11673 Plant ful
17	1325.5	67.9	372	3	AAG33123 Zea mays
18	1325.5	67.9	372	4	AAB48044 Signal tr
19	1320.5	67.9	380	8	ADY11385 Plant ful
20	1320.5	67.6	358	3	AAG33124 Zea mays
21	1316.5	67.4	376	3	AAG04672 Arabidops
22	1279	65.5	371	3	AAG45420 Arabidops
23	1232.5	63.1	373	8	ADT0480 Plant pol
24	1230	63.0	373	3	AAG30672 Arabidops

25	1210.5	62.0	372	3	AAG42613 Arabidops
26	1210.5	62.0	406	3	AAG42612 Arabidops
27	1208.5	61.9	372	3	AAG06702 Arabidops
28	1208.5	61.9	379	3	AAG06701 Arabidops
29	1173.5	60.1	354	3	AAG30978 Arabidops
30	1103.5	56.5	311	5	AAM52837 Physcomit
31	1074.5	55.0	216	8	ADX73133 Plant ful
32	1031.5	52.8	280	3	AAG04673 Arabidops
33	1020.5	52.3	280	3	AAG33125 Zea mays
34	1015	52.0	366	3	AAG44681 Zea mays
35	1015	52.0	367	3	AAG44680 Zea mays
36	1015	52.0	369	3	AAG44679 Zea mays
37	1015	52.0	369	7	ABW74137 DNA clone
38	1014	51.9	369	4	AAB48043 Signal tr
39	1003.5	51.4	370	8	ADT60889 Plant pol
40	1003	51.4	367	3	AAG44793 Zea mays
41	1003	51.4	368	3	AAG44792 Zea mays
42	1003	51.4	368	3	AAG35746 Zea mays
43	1003	51.4	370	3	AAG44791 Zea mays
44	1003	51.4	370	3	AAG35745 Zea mays
45	1003	51.4	370	4	AAB48045 Signal tr

## ALIGNMENTS

RESULT 1  
ADT02330  
ID ADT02330 standard; protein; 368 AA.  
XX  
AC ADT02330;  
XX  
-DT 13-JAN-2005 (first entry)  
XX  
DE Rice mitogen-activated protein kinase 5a (MAPK5a) polypeptide.  
XX  
KW Rice; mitogen-activated protein kinase 5a; MAPK5; MAPK5a;  
KW abiotic stress tolerance; biotic stress tolerance; drought; temperature;  
KW salinity; plant; enzyme.  
XX  
OS Oryza sativa.  
XX  
PH Key Location/Qualifiers  
FT Misc-difference 218 /note= "Encoded by ATGCAC"  
FT  
XX  
PN US2004209325-A1.  
XX  
PD 21-OCT-2004.  
XX  
PF 31-JAN-2004; 2004US-00768886.  
XX  
PR 31-JAN-2003; 2003US-0444249P.  
XX  
PA (YANG/) YANG Y.  
XX  
PA (XIONG/) XIONG L.  
XX  
Y Yang Y, Xiong L;  
XX  
WPI; 2004-747214/73.  
XX  
N-PSDB; ADT02339.  
XX  
PT New isolated nucleic acid molecule encoding a mitogen-activated protein  
PT kinase-5 (MAPK5) polypeptide, useful for increasing tolerance to abiotic  
PT and biotic stresses in plants.  
XX  
PS Claim 24; SEQ ID NO 2; 36pp; English.  
XX  
CC The invention relates to a rice mitogen-activated protein kinase 5  
CC (MAPK5) polypeptides and the polynucleotides encoding them. The invention  
CC also relates to an antibody that specifically binds to a peptide  
CC consisting of a C-terminal portion of a MAPK5 polypeptide, a transgenic  
CC plant transformed by a polynucleotide encoding a MAPK5 orthologue where



CC over expression of the MAPK5 orthologue in the plant results in increased  
 CC tolerance to abiotic stress compared to a wild-type plant and a method  
 CC for evaluating a plant for tolerance to abiotic stress comprising  
 CC treating a plant with abiotic stress, isolating a MAPK5 protein from the  
 CC plant, detecting MAPK5 activity and evaluating the increase or decrease  
 CC in MAPK5 activity in the plant where the increase in MAPK5 activity  
 CC indicates the plant is tolerant to abiotic stress. The methods and  
 CC compositions of the present invention are useful for increasing tolerance  
 CC to abiotic and biotic stress in plants using MAPK5, where the abiotic  
 CC stress is drought, temperature or salinity and the biotic stress is from  
 CC pathogenic bacteria, viruses, nematodes and insects. This sequence  
 CC represents the rice MAPK5a polypeptide of the invention.

XX Sequence 368 AA;

Query Match 100.0%; Score 1953; DB 8; Length 368;

Best Local Similarity 100.0%; Pred. No. 8.5e-192;

Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGAPVAEPRPTWTHGGRVLLYDFGNKEVTNKYQPPIMPIGRGAYGIVCSVMNPETRE 60

DB 1 MDGAPVAEPRPTWTHGGRVLLYDFGNKEVTNKYQPPIMPIGRGAYGIVCSVMNPETRE 60

QY 61 MVAIKKIANAFNNDMDAKRTLRREIKLRLHLDHENIIGIRDVIPPPIQAFNDVVIATELM 120

DB 61 MVAIKKIANAFNNDMDAKRTLRREIKLRLHLDHENIIGIRDVIPPPIQAFNDVVIATELM 120

QY 121 DTDLHHIIRSNQELSEHCQFYQLRGLKYTHSANVTHRDLPKPSNLLNANCDLKICD 180

DB 121 DTDLHHIIRSNQELSEHCQFYQLRGLKYTHSANVTHRDLPKPSNLLNANCDLKICD 180

QY 181 FGLARPSSSDMTVEVVTWYRAPPELLNSTDYSAADVWSVGCIFMELINRQPLPFGRD 240

DB 181 FGLARPSSSDMTVEVVTWYRAPPELLNSTDYSAADVWSVGCIFMELINRQPLPFGRD 240

QY 241 HHQMLITEVIGTPTDDELGFIRNEDARKYMRHLPQYPRRTFASMPFRVQPAALDLIER 300

DB 241 HHQMLITEVIGTPTDDELGFIRNEDARKYMRHLPQYPRRTFASMPFRVQPAALDLIER 300

QY 301 MLTFNPLQRTVEALDHPYLERLHDIADPEICLPESFDPEQKALNEDQKLIIFNEAI 360

DB 301 MLTFNPLQRTVEALDHPYLERLHDIADPEICLPESFDPEQKALNEDQKLIIFNEAI 360

QY 361 EMNPNI9Y 368

DB 361 EMNPNI9Y 368

RESULT 2

AAG34157

ID AAG34157 standard; protein; 374 AA.

XX AAG34157;

AC AAG34157;

XX 18-OCT-2000 (first entry)

DT Zea mays protein fragment SEQ ID NO: 41518.

DE Zea mays subsp. mays.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

FR 05-MAR-1999; 99US-0123180P.

PR 09-MAR-1999; 99US-0123548P.

PR 23-MAR-1999; 99US-0125788P.

PR 25-MAR-1999; 99US-0126264P.

PR 29-MAR-1999; 99US-0126785P.

PR 01-APR-1999; 99US-0127462P.

PR 06-APR-1999; 99US-0128234P.

PR 08-APR-1999; 99US-0128714P.

PR 16-APR-1999; 99US-0129845P.

PR 19-APR-1999; 99US-0130077P.

PR 21-APR-1999; 99US-0130449P.

PR 23-APR-1999; 99US-0130510P.

PR 23-APR-1999; 99US-0130691P.

PR 28-APR-1999; 99US-0131449P.

PR 30-APR-1999; 99US-0132048P.

PR 30-APR-1999; 99US-0132407P.

PR 04-MAY-1999; 99US-0132484P.

PR 05-MAY-1999; 99US-0132485P.

PR 06-MAY-1999; 99US-0132486P.

PR 06-MAY-1999; 99US-0132487P.

PR 07-MAY-1999; 99US-0132863P.

PR 11-MAY-1999; 99US-0134256P.

PR 14-MAY-1999; 99US-0134218P.

PR 14-MAY-1999; 99US-0134219P.

PR 14-MAY-1999; 99US-0134221P.

PR 14-MAY-1999; 99US-0134222P.

PR 14-MAY-1999; 99US-0134370P.

PR 18-MAY-1999; 99US-0134768P.

PR 19-MAY-1999; 99US-0134941P.

PR 20-MAY-1999; 99US-0135124P.

PR 21-MAY-1999; 99US-0135353P.

PR 24-MAY-1999; 99US-0135629P.

PR 25-MAY-1999; 99US-0136021P.

PR 27-MAY-1999; 99US-0136392P.

PR 28-MAY-1999; 99US-0136782P.

PR 01-JUN-1999; 99US-0137222P.

PR 03-JUN-1999; 99US-0137528P.

PR 04-JUN-1999; 99US-0137502P.

PR 07-JUN-1999; 99US-0137724P.

PR 08-JUN-1999; 99US-0138094P.

PR 10-JUN-1999; 99US-0138540P.

PR 10-JUN-1999; 99US-0138847P.

PR 14-JUN-1999; 99US-0139119P.

PR 16-JUN-1999; 99US-0139452P.

PR 16-JUN-1999; 99US-0139453P.

PR 17-JUN-1999; 99US-0139492P.

PR 18-JUN-1999; 99US-0139454P.

PR 18-JUN-1999; 99US-0139455P.

PR 18-JUN-1999; 99US-0139456P.

PR 18-JUN-1999; 99US-0139457P.

PR 18-JUN-1999; 99US-0139458P.

PR 18-JUN-1999; 99US-0139459P.

PR 18-JUN-1999; 99US-0139460P.

PR 18-JUN-1999; 99US-0139461P.

PR 18-JUN-1999; 99US-0139462P.

PR 18-JUN-1999; 99US-0139463P.

PR 18-JUN-1999; 99US-0139750P.

PR 18-JUN-1999; 99US-0139763P.

PR 21-JUN-1999; 99US-0139817P.

PR 22-JUN-1999; 99US-0139899P.

PR 23-JUN-1999; 99US-0140353P.

PR 24-JUN-1999; 99US-0140354P.

PR 24-JUN-1999; 99US-0140695P.

PR 28-JUN-1999; 99US-0140823P.

PR 29-JUN-1999; 99US-0140991P.

PR 30-JUN-1999; 99US-0141287P.

PR 01-JUL-1999; 99US-0141842P.

PR 01-JUL-1999; 99US-0142154P.

PR 02-JUL-1999; 99US-0142055P.

PR 06-JUL-1999; 99US-0142390P.

PR 08-JUL-1999; 99US-0142803P.

PR 09-JUL-1999; 99US-0142920P.

PR 12-JUL-1999; 99US-0142977P.

PR 13-JUL-1999; 99US-0143542P.

PR 14-JUL-1999; 99US-0143624P.

PR 15-JUL-1999; 99US-0144005P.

[illegible]

RESULT 3  
AAB48046  
ID AAB48046 standard; protein; 374 AA.  
XX  
AC  
XX AAB48046;  
AC  
XX  
DT 19-MAR-2001 (first entry)  
XX

DE	Signal transduction protein.	
XX	Zea mays; maize; signal transduction protein; phytohormone; ethylene;	
KW	auxin; cytokinin; gibberellin; immunogen.	
XX		
OS	Zea mays.	
XX		
PN	WO200070059-A2.	
XX		
PD	23-NOV-2000.	
XX		
PF	28-APR-2000; 2000WO-US011687.	
XX		
PR	14-MAY-1999; 99US-0134292P.	
XX		
PR	08-JUL-1999; 99US-0142996P.	
XX		
PA	(PION-) PIONEER HI-BRED INT INC.	
XX		
PI	Helentjaris TG;	
XX		
DR	WPI; 2001-031929/04.	
DR	N-PSDB; AAC64259.	
XX		
PT	New signal transduction nucleic acids and encoded proteins useful for	
PT	regulating phytohormone expression, including ethylene, auxins,	
PT	cytokinins and gibberellin, to provide control of plant response to	
PT	environmental stresses.	
XX		
PS	Claim 13; Page 91; 136pp; English.	
XX		
CC	The invention provides Zea mays signal transduction proteins and encoding	
CC	nucleotide sequences. The nucleic acids are useful for regulating	
CC	expression of phytohormones, including ethylene, auxins, cytokinins, and	
CC	gibberellin, to effect developmental changes in plants and provide	
CC	control of plant response to environmental stresses. They may also be	
CC	used as probes or amplification primers in the detection, quantitation or	
CC	isolation of gene transcripts, for detecting mutations in the gene, for	
CC	monitoring upregulation of expression or changes in enzyme activity in	
CC	screening assays of compounds, for detection of any number of allelic	
CC	variants, or for site-directed mutagenesis in eukaryotic cells. They may	
CC	further be used for recombinant expression of their encoded polypeptides,	
CC	as immunogens in the preparation or screening of antibodies, and in sense	
CC	or antisense suppression of genes in a host cell, tissue or plant. The	
CC	proteins may be used in assays for enzyme agonists or antagonists, as	
CC	immunogens or antigens to obtain antibodies specifically immunoreactive	
CC	with the proteins. The present sequence represents a signal transduction	
CC	protein of the invention	
XX		
SQ	Sequence 374 AA;	
	Query Match 92.1%; Score 1798.5; DB 4; Length 374;	
	Best Local Similarity 90.8%; Pred. No. 6.9e-176;	
	Matches 335; Conservative 20; Mismatches 13; Indels 1; Gaps 1;	
QY	1 MDGAPVAEPRFTMTGCGRYLLYDIFGNKPEVTNKYOPPIGCGAYGIVCSVMNPETRE 60	
DB	6 VDGAPVAEPRFTMTGCGRYLLYDIFGNKPEVTNKYOPPIGCGAYGIVCSVMNPETRE 65	
QY	61 MVAIKKIANAFNDMDAKTLEIKLRLHLDHNIIGIRDVIPPPIPOAFNDVYIATELM 120	
DB	66 MVAIKKIANAFNDMDAKTLEIKLRLHLDHNIIGIRDVIPPPIPOAFNDVYIATELM 125	
QY	121 DTDLHHIIRSNQELSEHCQFLYQLRLGKLYTHSANVTHRLKPSNLLNANCDLKICD 180	
DB	126 DTDLHHIIRSNQELSEHCQFLYQLRLGKLYTHSANVTHRLKPSNLLNANCDLKICD 185	
QY	181 FGLARPSSSDMMTEYVTVTRWYRAPELLNSTDYSAA-DVWSVGCIFMELINRQPLFPGR 239	
DB	186 FGLARPSSSDMMTEYVTVTRWYRAPELLNSTDYSAAIDVWSVGCIFMELINRQPLFPGR 245	
QY	240 DHMHQRLITEVIGTDDDELGFIREDARKYMRHLPOYPRRTFASMPFRVQPAALDLIE 299	
DB	246 DHMHQRLITEVIGTDDDELGFIREDARKYMRHLPOYPRRTFASMPFRVQPAALDLIE 305	
QY	300 RMLTFNPLQRTVBEALDHPYLERLHDIADBPICLEPFSDFEQKALNEDQMKQLIFNEA 359	
DB	306 RMLTFNPLQRTVBEALDHPYLERLHDIADBPICLEPFSDFEQKALNEDQMKQLIFNEA 365	
QY	360 IEMPNIRY 368	
DB	366 MELNPNRY 374	
XX		
RESULT 4		
AAG34158		
ID	AAG34158 standard; protein; 330 AA.	
XX		
AC	AAG34158;	
XX		
DT	18-OCT-2000 (first entry)	
XX		
DE	Zea mays protein fragment SEQ ID NO: 41519.	
XX		
KW	Protein identification; signal transduction pathway; metabolic pathway;	
KW	hybridisation assay; genetic mapping; gene expression control; promoter;	
KW	termination sequence; corn.	
XX		
OS	Zea mays subsp. mays.	
XX		
PN	EP1033405-A2.	
XX		
PD	06-SEP-2000.	
XX		
PF	25-FEB-2000; 2000EP-00301439.	
XX		
PR	25-FEB-1999; 99US-0121825P.	
PR	09-MAR-1999; 99US-0123180P.	
PR	09-MAR-1999; 99US-0123548P.	
PR	23-MAR-1999; 99US-0125788P.	
PR	25-MAR-1999; 99US-0126264P.	
PR	29-MAR-1999; 99US-0126785P.	
PR	01-APR-1999; 99US-0127462P.	
PR	06-APR-1999; 99US-0128234P.	
PR	08-APR-1999; 99US-0128714P.	
PR	16-APR-1999; 99US-0129845P.	
PR	19-APR-1999; 99US-0130077P.	
PR	21-APR-1999; 99US-0130449P.	
PR	23-APR-1999; 99US-0130510P.	
PR	23-APR-1999; 99US-0130891P.	
PR	28-APR-1999; 99US-0131449P.	
PR	30-APR-1999; 99US-0132048P.	
PR	30-APR-1999; 99US-0132407P.	
PR	04-MAY-1999; 99US-0132484P.	
PR	05-MAY-1999; 99US-0132485P.	
PR	06-MAY-1999; 99US-0132486P.	
PR	06-MAY-1999; 99US-0132487P.	
PR	07-MAY-1999; 99US-0132863P.	
PR	11-MAY-1999; 99US-0134256P.	
PR	14-MAY-1999; 99US-0134218P.	
PR	14-MAY-1999; 99US-0134219P.	
PR	14-MAY-1999; 99US-0134221P.	
PR	14-MAY-1999; 99US-0134370P.	
PR	18-MAY-1999; 99US-0134768P.	
PR	19-MAY-1999; 99US-0134941P.	
PR	20-MAY-1999; 99US-0135124P.	
PR	21-MAY-1999; 99US-0135353P.	
PR	24-MAY-1999; 99US-0135629P.	
PR	25-MAY-1999; 99US-0136021P.	
PR	27-MAY-1999; 99US-0136392P.	
PR	28-MAY-1999; 99US-0136782P.	
PR	01-JUN-1999; 99US-0137222P.	
PR	03-JUN-1999; 99US-0137528P.	
PR	04-JUN-1999; 99US-0137502P.	
PR	07-JUN-1999; 99US-0137724P.	
PR	08-JUN-1999; 99US-0138094P.	
PR	10-JUN-1999; 99US-0138540P.	



Db	1	MPIGRGAYGIVCSVMNSETKEWVAIKKIANAFDNHMDAKRTLREIKLRLHLDHENIIGTR	60	PR	19-MAY-1999;	99US-0134941P.
Qy	100	DVTPPPIPQAFNDVYIATLMDTDLHHIIRSNOELSEHCQYFLYQILRGLKYIHSANVI	159	PR	20-MAY-1999;	99US-0135124P.
Db	61	DVTPPPVPQAFNDVIGTELMDTDLHHIIRSNOELSEHSQYFLYQILRGLKYIHSANVI	120	PR	21-MAY-1999;	99US-0135353P.
Qy	160	HRDLKPSNLLNANCDLKI CDFGLARPSSESMDMTYVTVRWYRAPPELLNSTDYSAAD	218	PR	24-MAY-1999;	99US-0135629P.
Db	121	HRDLKPSNLLNANCDLKI CDFGLARPSSESMDMTYVTVRWYRAPPELLNSTDYSAAD	180	PR	25-MAY-1999;	99US-0136021P.
Qy	219	VNSVGCIFMELINRQPLFPGRDHMHQMLITEVIGTPTDDELGFIRNEDARKYMRHLPOY	278	PR	27-MAY-1999;	99US-0136392P.
Db	181	VNSVGCIFMELINRQPLFPGRDHMHQMLITEVIGTPTDDELGFIRNEDARKYMRHLPOF	240	PR	28-MAY-1999;	99US-0136782P.
Qy	279	PRTFASMPFRVQPAALDIERMLTFNPLQRITVEBALDHPYLERLHDIADEPICLEPFS	338	PR	01-JUN-1999;	99US-0137222P.
Db	241	PRPFVSLFPRMQPVALDIERMLTFNPLQRITVEEALHPYLERLHDVADEPICTDPS	300	PR	03-JUN-1999;	99US-0137528P.
Qy	339	FDPEQKALNEDQMKQLIFNEAIEIENPNIRY	368	PR	04-JUN-1999;	99US-0137502P.
Db	301	FDPEQKALNEDQMKQLIFNEAIEIENPNIRY	330	PR	07-JUN-1999;	99US-0137724P.
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AAG34159				PR	10-JUN-1999;	99US-0138540P.
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AC				PR	14-JUN-1999;	99US-0139119P.
XX				PR	16-JUN-1999;	99US-0139453P.
DT				PR	17-JUN-1999;	99US-0139492P.
XX				PR	18-JUN-1999;	99US-0139458P.
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XX				PR	18-JUN-1999;	99US-0139460P.
KW				PR	18-JUN-1999;	99US-0139461P.
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XX				PR	18-JUN-1999;	99US-0139457P.
OS				PR	18-JUN-1999;	99US-0139458P.
PN				PR	18-JUN-1999;	99US-0139750P.
PD				PR	18-JUN-1999;	99US-0139763P.
XX				PR	21-JUN-1999;	99US-0139817P.
XX				PR	22-JUN-1999;	99US-0139899P.
DE				PR	23-JUN-1999;	99US-0140353P.
KW				PR	23-JUN-1999;	99US-0140354P.
KW				PR	24-JUN-1999;	99US-0140695P.
KW				PR	28-JUN-1999;	99US-0140823P.
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PN				PR	01-JUL-1999;	99US-0141842P.
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XX				PR	09-JUL-1999;	99US-0142920P.
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XX				PR	13-JUL-1999;	99US-0143542P.
XX				PR	14-JUL-1999;	99US-0143624P.
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XX				PR	19-JUL-1999;	99US-0144325P.
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XX				PR	19-JUL-1999;	99US-0144332P.
XX				PR	19-JUL-1999;	99US-0144333P.
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XX				PR	19-JUL-1999;	99US-0144335P.
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XX				PR	20-JUL-1999;	99US-0144884P.
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XX				PR	21-JUL-1999;	99US-0145088P.
XX				PR	22-JUL-1999;	99US-0145085P.
XX				PR	22-JUL-1999;	99US-0145087P.
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XX				PR	23-JUL-1999;	99US-0145218P.
XX				PR	23-JUL-1999;	99US-0145224P.
XX				PR	26-JUL-1999;	99US-0145276P.
XX				PR	27-JUL-1999;	99US-0145913P.
XX				PR	27-JUL-1999;	99US-0145918P.
XX				PR	27-JUL-1999;	99US-0145919P.

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PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
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PR 05-AUG-1999; 99US-0147192P.
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PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
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PR 23-AUG-1999; 99US-0149802P.
PR 23-AUG-1999; 99US-0149930P.
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PR 26-AUG-1999; 99US-0150884P.
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PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 28-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
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PR 13-OCT-1999; 99US-0159295P.
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PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
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PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.

PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 79.7%; Score 1557.5; DB 3; Length 316;
Best Local Similarity 92.7%; Pred.No. 3.5e-151;
Matches 293; Conservative 12; Mismatches 10; Indels 1; Gaps 1;

QY 54 MNFETREVAIKKIANAFNNDMAKRTLRREIKLRLHLDHENIIGIRDVIPPPIPOAFNDV 113
DB 1 MNSETKEMVAIKKIANAFNNDMAKRTLRREIKLRLHLDHENIIGIRDVIPPVPQAFNDV 60
QY 114 YIATELMDTDLHHIIRSNQELSEHCQVFLYQILRGLKYIHSANVHRLDKPSNLLNAN 173
DB 61 YIGTELMDTDLHHIIRSNQELSEHSQVFLYQILRGLKYIHSANVHRLDKPSNLLNAN 120
QY 174 CDLKICDFGLARPSSESDMTTEYVVRWYRAPPELLNSTDYSAA-DVMSVGCIFMELINR 232
DB 121 CDLKICDFGLARPSSESDMTTEYVVRWYRAPPELLNSTDYSAAIDVMSVGCIFMELINR 180
QY 233 QPLFGGRDHMQRLITEVIGTPTDELGFIRNEDARKYMRHLPOVPRRTFASMPFRVOP 292
DB 181 QPLFGGRDHMQRLITEVIGTPTDELGFIRNEDARKYMRHLPOVPRRTFASMPFRVOP 240
QY 293 AALDLIERMLTNPLQRTIVTEBALDHPYLERLHLDIADEPICLEPFSDFEQKALNEDQMK 352
DB 241 VALDLIERMLTNPLQRTIVTEBALDHPYLERLHLDVADEPCTDPFSDFEQQALETQDKM 300
QY 353 QLIFNEAIEIEMNPRIY 368
DB 301 QLIFNEAIEIEMNPRIY 316

RESULT 6
AAW15512
ID AAW15512 standard; protein; 375 AA.
XX
AC AAW15512;
XX
DT 04-JUN-1997 (first entry)
XX
DE MAP kinase #1.
KW Mitogen activated protein kinase; MAP; infectious specific protein;
KW plant; jasmonate acid.
XX
OS Synthetic.
XX
PN JP09065881-A.
PD 11-MAR-1997.
XX
PF 29-AUG-1995; 95JP-00220935.
XX
PR 29-AUG-1995; 95JP-00220935.
XX
PA (NORQ ) NORINSUISANSO NOGYO SEIBUTSU SHIGEN.
XX
DR WPI; 1997-220416/20.
XX
DR N-PSDB; AAT60349.
XX
PT Wound-stress inducible MAP kinase - used to regulate the synthesis of
PT jasmonate acid.
PS Claim 2; Page 13-14; 21pp; Japanese.
XX
AAW15512 and AAW15513 represent the mitogen activated protein (MAP)
CC kinases of the invention. This sequence contains the T-E-Y sequence, in
CC which the threonine and tyrosine residues are phosphorylated to activate
CC the protein at residues201-203. The MAP kinase and its gene can be used
```

CC to regulate the synthesis of jasmonic acid and the synthesis of a group of  
 CC infectious specific proteins. By introducing the MAP kinase gene into a  
 CC plant, thereby inducing expression of the mRNA for MAP kinase (or its  
 CC antisense RNA), the synthesis of jasmonic acid and a group of infectious  
 CC specific proteins can be regulated in the plant

XX Sequence 375 AA;

Query Match 75.4%; Score 1472.5; DB 2; Length 375;  
 Best Local Similarity 72.5%; Pred. No. 2.5e-142;  
 Matches 263; Conservative 58; Mismatches 41; Indels 1; Gaps 1;  
 QY 3 GAPVABRPWTHTGGRYLLYDIFGNKPEVTNKKYQPPIMPICRGAYGIVCSVMNFETREM 62  
 Db 10 GGGQFPDPFVSLTHGGQYVQDFICGNPFETTKYRPPIMPICRGAYGIVCSVLNTELEW 69  
 QY 63 AIKKIANAFNNDMDAKETLREIKLRLHDHENIIGIRDVTPPIPOAFNDVYIATELMDT 122  
 Db 70 AVKIANAFDIYMDAKETLREIKLRLHDHENIIGIRDVTPPIPOAFNDVYIATELMDT 129  
 QY 123 DLHHIIRSNQELSEHCQYFLYQILRLGLKYIHSANVHRLDKPSNLLNANCDLKICDFG 182  
 Db 130 DLHQIIRSNQELSEHCQYFLYQILRLGLKYIHSANVHRLDKPSNLLNANCDLKICDFG 189  
 QY 183 LARPSSSDMMTEYVVTWTRAPPELLNSTDYSAADVWSVGCIFMELINRQPLFPGRDH 241  
 Db 190 LARPNIENENMTEYVVTWTRAPPELLNSTDYSAADVWSVGCIFMELNKRKPLFGKDH 249  
 QY 242 MHQMLRITVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPRVPQALDLIERM 301  
 Db 250 VHQRLTELGITPTDDELGFQNEADAKRYRQLPOHROOLAEVFPVHNPPLAIDLVDKM 309  
 QY 302 LTFNPLQRIITVEEALDHPYLERLHDIADEPICLEPFSDFEQKALNEDQMKQIFNEAIE 361  
 Db 310 LTFDPTRRITVEEALDHPYLAHLADAGDEPICVPFSDFEQQIGEEQIKDIYQEALS 369  
 QY 362 MNP 364  
 Db 370 LNP 372

RESULT 7  
 AAB48048  
 ID AAB48048 standard; protein; 398 AA.

XX AAB48048;

XX 19-MAR-2001 (first entry)

XX Signal transduction protein.

XX Zea mays; maize; signal transduction protein; phytohormone; ethylene;  
 XX auxin; cytokinin; gibberellin; immunogen.

XX Zea mays.

XX WO200070059-A2.

XX 23-NOV-2000.

XX 28-APR-2000; 2000WO-US011687.

XX 14-MAY-1999; 99US-0134292P.

XX 08-JUL-1999; 99US-0142996P.

XX (PION-) PIONEER HI-BRED INT INC.

XX Helentjaris TG;

XX WPI; 2001-031929/04.

XX N-PSDB; AAC84265.

XX New signal transduction nucleic acids and encoded proteins useful for

PT regulating phytohormone expression, including ethylene, auxins,  
 PT cytokinins and gibberellin, to provide control of plant response to  
 PT environmental stresses.

PS Claim 13; Page 97; 126pp; English.

XX The invention provides Zea mays signal transduction proteins and encoding  
 CC nucleotide sequences. The nucleic acids are useful for regulating  
 CC expression of phytohormones, including ethylene, auxins, cytokinins, and  
 CC gibberellin, to effect developmental changes in plants and provide  
 CC control of plant response to environmental stresses. They may also be  
 CC used as probes or amplification primers in the detection, quantitation or  
 CC isolation of gene transcripts, for detecting mutations in the gene, for  
 CC monitoring upregulation of expression or changes in enzyme activity in  
 CC screening assays of compounds, for detection of a number of allelic  
 CC variants, or for site-directed mutagenesis in eukaryotic cells. They may  
 CC further be used for recombinant expression of their encoded polypeptides,  
 CC as immunogens in the preparation or screening of antibodies, and in sense  
 CC or antisense suppression of genes in a host cell, tissue or plant. The  
 CC proteins may be used in assays for enzyme agonists or antagonists, as  
 CC immunogens or antigens to obtain antibodies specifically immunoreactive  
 CC with the proteins. The present sequence represents a signal transduction  
 CC protein of the invention

XX Sequence 398 AA;

Query Match 74.2%; Score 1448.5; DB 4; Length 398;  
 Best Local Similarity 73.4%; Pred. No. 8.1e-140;  
 Matches 268; Conservative 51; Mismatches 43; Indels 3; Gaps 3;  
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 QY 62 VAIKIANAFNNDMDAKETLREIKLRLHDHENIIGIRDVTPPIPOAFNDVYIATELMD 121  
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 Db 213 GLARTTSETDFMTYVVTWTRAPPELLNSTDYSAADVWSVGCIFMELMDRKLFPGRD 272  
 QY 241 HMQMLRITVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPRVPQALDLIER 300  
 Db 273 HVHQRLLMELIGTPTNEADLDFV-NENARRYIRQLPCHAROSFPEKFPVHNPPLAIDLVEK 331  
 QY 301 MLTFNPLQRIITVEEALDHPYLERLHDIADEPICLEPFSDFEQKALNEDQMKQIFNEAI 360  
 Db 332 MLTFDPTRRITVEEALDHPYLAHLADISDEPVCSPFSDFEQHALSEQMDLIYQEAL 391  
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 Db 392 AFNP 396

RESULT 8

ID AAG31654 standard; protein; 382 AA.

XX AAG31654;

XX 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 38049.

XX Protein identification; signal transduction pathway; metabolic pathway;  
 KW hybridisation assay; genetic mapping; gene expression control; promoter;  
 KW termination sequence.



OS Arabidopsis thaliana.  
XX EP1033405-A2.  
XX 06-SEP-2000.  
XX 25-FEB-2000; 2000EP-00301439.  
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QY	53	VNNPFTREMYAIKKIANAFNNDMAKRTREIKLRHLDHENIIGTRDVIPTPIPOAFND 112
DB	67	AMMSETNESVAIKKIANAFNPKIDAKTREIKLRHMDHENIVAIRDIIPPLRNAFND 126
QY	113	VYIATELMDYDLHHIIRSNQELSEHCQVFLYQILRGLKYIHSANVIHRDLKPSNLLNA 172
DB	127	VYIAYELMDYDLHIIIRSNQALSEHCQVFLYQILRGLKYIHSANVLRDLKPSNLLNA 186
QY	173	NCDLKICDFGLARPPSSDMYTYVTRWTRAPPELLNSTDYAAA-DVMSVGCIFMELIN 231
DB	187	NCDLKICDFGLARVTSSEDPMTYVTVWTRAPPELLNSDYTAADVMSVGCIFMELMD 246
QY	232	RQLPFCRDHMHOMRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPRVQ 291
DB	247	RKELFCRDHMHQRLMELIGTPSSELEFL-ENAKRYIRQLPPYRQSTIDKPEPTVH 305
QY	292	PAALDLIERMLTFNPLQRIITVEBALDHPYLERLHDADEPFCLEPFSFDFEQKALNEDQM 351
DB	306	PLAIDLIERKMLTFDPRRITVLDALAHPLYLNSLHDSDEPECTIPNFDFENHALSEEQM 365
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XX	DT	17-OCT-2000 (first entry)
XX	DE	Arabidopsis thaliana protein fragment SEQ ID NO: 38048.
KW	Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.	
XX	OS	Arabidopsis thaliana.
XX	PN	EP1033405-A2.
XX	PD	06-SEP-2000.
XX	PF	25-FEB-2000; 2000EP-00301439.
XX	PR	25-FEB-1999; 99US-0121825P.
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PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161992P.  
PR 28-OCT-1999; 99US-0161993P.  
PR 29-OCT-1999; 99US-0162142P.

Query Match 73.8%; Score 1442; DB 3; Length 395;

Best Local Similarity 72.4%; Pred. No. 3.7e-139;

Matches 270; Conservative 46; Mismatches 45; Indels 12; Gaps 3;

QY 3 GAPVAERFP-----TWTHGGRYLLYDIFGNKFEVTNKYQPPIMPGRGAYGIVCS 52

Db 20 GPPAAAPSQMPGCIENIPATLSHGGRFIQYINIFGNIFETAKYKPIIMPGRGAYGIVCS 79

QY 53 VMNFETRENVAKKIANAFNNDMDAKRTLREIKLLRHLRHDENIGIRDVIPPPIPOAFND 112

Db 80 AMNSETNESVAIKKIANAFDNKDARTLREIKLLRHDENIVAIRDIIPPPLRNAFND 139

QY 113 VYIATELMDTDLHHTRSNQELSEHCQYFLYQILRGLKYIHSANVHRDLKPSNLLNA 172

```

Db      140  VYIAVELMDTLHQIIRSNQALSEEHCOFLYQILRGLKYIHSANYLHRDLKPSNLLNA 199
Qy      173  NCDLKICDFGLARPSSSDMTVEYVYTRVRAPELLNSTDYSAADVMSVGCIFMELIN 231
Db      200  NCDLKICDFGLARVTSESDFMTEYVYTRVRAPELLNSDTRAIDVMSVGCIFMELMD 259
Qy      232  RQPLFPGRDHMQRLITEVIGTPTDDELGFIRNEDARKYMRHLPOYPRRTFASMPRVQ 291
Db      260  RKPLFPGRDHVHQRLRLMELIGTSPSEEELEFTNENAKYIRQLPPYRQSIITDKPPTVH 318
Qy      292  PAALDIERMLTFNPQRIITVEALDHPYLERLHDIADEPICLEPSPDFEQKALNEDQM 351
Db      319  PLAIDLIERKMLTFDPERRITVLDALAHPLYLSLHDSDEPCTIPNPFDFENHALSEEQM 378
Qy      352  KOLIFNEAJEMNP 364
Db      379  KELIYREALAFNP 391

RESULT 10
AAG31655
ID  AAG31655 standard; protein; 366 AA.
XX  AAG31655;
AC
XX
DT  17-OCT-2000 (first entry)
DE  Arabidopsis thaliana protein fragment SEQ ID NO: 38050.
XX
KW  Protein identification; signal transduction pathway; metabolic pathway;
KW  hybridisation assay; genetic mapping; gene expression control; promoter;
KW  termination sequence.
XX
OS  Arabidopsis thaliana.
XX
PN  EP1033405-A2.
XX
PD  06-SRP-2000.
XX
PF  25-FEB-2000; 2000BP-00301439.
XX
PR  25-FEB-1999; 99US-0121825P.
PR  05-MAR-1999; 99US-0123180P.
PR  09-MAR-1999; 99US-01233548P.
PR  23-MAR-1999; 99US-01257888P.
PR  25-MAR-1999; 99US-0126264P.
PR  29-MAR-1999; 99US-0126785P.
PR  01-APR-1999; 99US-0127462P.
PR  06-APR-1999; 99US-0128234P.
PR  08-APR-1999; 99US-0128714P.
PR  16-APR-1999; 99US-0129845P.
PR  19-APR-1999; 99US-0130077P.
PR  21-APR-1999; 99US-0130449P.
PR  23-APR-1999; 99US-0130510P.
PR  28-APR-1999; 99US-0130891P.
PR  30-APR-1999; 99US-0131449P.
PR  30-APR-1999; 99US-0132048P.
PR  04-MAY-1999; 99US-0132407P.
PR  05-MAY-1999; 99US-0132484P.
PR  06-MAY-1999; 99US-0132485P.
PR  06-MAY-1999; 99US-0132486P.
PR  07-MAY-1999; 99US-0132487P.
PR  11-MAY-1999; 99US-0132863P.
PR  14-MAY-1999; 99US-0134256P.
PR  14-MAY-1999; 99US-0134218P.
PR  14-MAY-1999; 99US-0134219P.
PR  14-MAY-1999; 99US-0134221P.
PR  18-MAY-1999; 99US-0134370P.
PR  19-MAY-1999; 99US-01343768P.
PR  20-MAY-1999; 99US-0134941P.
PR  21-MAY-1999; 99US-0135124P.
PR  21-MAY-1999; 99US-0135353P.
PR  24-MAY-1999; 99US-0135629P.
PR  25-MAY-1999; 99US-0136021P.
PR  27-MAY-1999; 99US-0136392P.
PR  28-MAY-1999; 99US-0136782P.
PR  01-JUN-1999; 99US-0137222P.
PR  03-JUN-1999; 99US-0137528P.
PR  04-JUN-1999; 99US-0137502P.
PR  07-JUN-1999; 99US-0137724P.
PR  08-JUN-1999; 99US-0138094P.
PR  10-JUN-1999; 99US-0138540P.
PR  10-JUN-1999; 99US-0138847P.
PR  14-JUN-1999; 99US-0139119P.
PR  16-JUN-1999; 99US-0139452P.
PR  16-JUN-1999; 99US-0139453P.
PR  17-JUN-1999; 99US-0139492P.
PR  18-JUN-1999; 99US-0139454P.
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PR  18-JUN-1999; 99US-0139456P.
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PR  18-JUN-1999; 99US-0139458P.
PR  18-JUN-1999; 99US-0139459P.
PR  18-JUN-1999; 99US-0139460P.
PR  18-JUN-1999; 99US-0139461P.
PR  18-JUN-1999; 99US-0139462P.
PR  18-JUN-1999; 99US-0139463P.
PR  18-JUN-1999; 99US-0139750P.
PR  18-JUN-1999; 99US-0139763P.
PR  21-JUN-1999; 99US-0139817P.
PR  22-JUN-1999; 99US-0139899P.
PR  23-JUN-1999; 99US-0140353P.
PR  23-JUN-1999; 99US-0140354P.
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PR  28-JUN-1999; 99US-0140823P.
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PR  30-JUN-1999; 99US-0141287P.
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PR  14-JUL-1999; 99US-0143624P.
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PR  19-JUL-1999; 99US-0144335P.
PR  20-JUL-1999; 99US-0144352P.
PR  20-JUL-1999; 99US-0144632P.
PR  20-JUL-1999; 99US-0144884P.
PR  21-JUL-1999; 99US-0144814P.
PR  21-JUL-1999; 99US-0145086P.
PR  21-JUL-1999; 99US-0145088P.
PR  22-JUL-1999; 99US-0145085P.
PR  22-JUL-1999; 99US-0145087P.
PR  22-JUL-1999; 99US-0145089P.
PR  22-JUL-1999; 99US-0145192P.
PR  23-JUL-1999; 99US-0145145P.
PR  23-JUL-1999; 99US-0145218P.
PR  23-JUL-1999; 99US-0145224P.
PR  26-JUL-1999; 99US-0145276P.
PR  27-JUL-1999; 99US-0145913P.
PR  27-JUL-1999; 99US-0145918P.
PR  27-JUL-1999; 99US-0145919P.
PR  28-JUL-1999; 99US-0145951P.
PR  02-AUG-1999; 99US-0146386P.
PR  02-AUG-1999; 99US-0146388P.
```



CC kinase subdomains I to XI of serine/threonine kinases. The protein is  
 CC activated by an agent that induces a disease defence response in plants  
 CC by way of a signal transduction pathway that is at least partially  
 CC dependent on salicylic acid. Host plant cells transformed with a vector  
 CC containing a recombinant DNA molecule encoding the salicylic acid induced  
 CC MAP kinase is used to produce the protein recombinantly. The products can  
 CC be used to produce plants with increased disease resistance. The products  
 CC may also be used as a research tool to identify other proteins involved  
 CC in the hypersensitive response and systemic acquired response in plants  
 XX  
 XX Sequence 393 AA;

Query Match 73.7%; Score 1438.5; DB 2; Length 393;  
 Best Local Similarity 72.4%; Pred. No. 8.5e-139;  
 Matches 267; Conservative 50; Mismatches 45; Indels 7; Gaps 3;

QY 1 MDGAPVAEPTMTGGRVLLYDIFGNKPEVTNKYOPPIGPGAYGIVCSVMNPETRE 60  
 DB 30 MDNIPA-----TUSHGGRFIQYNIQNFIVETAKYKPPILPGKAYGIVCSALNSSETIE 84  
 QY 61 MVAIKKIANAFNNDMDAKRTLREIKLRLHLDHENIIGIRDVIPPPIPOAFNDVYIATELM 120  
 DB 85 NVAIKKIANAFDNKIDAKRTLREIKLRLHMDHENIVAIRDIPPPQREAFNDVYIAYELM 144  
 QY 121 DTLHHIIRSNQELSEHCQFYLIQILRGKYIHSANVIHRDLKPSNLLNANCDLKICD 180  
 DB 145 DTDLHQIIRSNQELSEHCQFYLIQILRGKYIHSANVLRDLKPSNLLNANCDLKICD 204  
 QY 181 FGLARPSSEDMTEYVTVTRWYRAPELLNSTDYSAA-DVWSVGCIFMELINRQPLPGR 239  
 DB 205 FGLARVTSDFMTEYVTVTRWYRAPELLNSTDYSAA-DVWSVGCIFMELINRQPLPGR 264  
 QY 240 DHMHQRLITEVIGTPTDDELGFIRNEDARKYMRHLPQYPRRTFASMPFRVOPAAALDLIE 299  
 DB 265 DHVQLRLMELIGTPEAEWEL-ENAKRYIQLPYRRQSFTKFPVHPTAIDLVE 323  
 QY 300 RMLTFNPLORITVEALDHPYLERLHDADEPICLEPFSDFEQKALNEDQMKLIENEA 359  
 DB 324 KMLTFDPRRITVEGALAHPLASLHDSIDEPICMTFSDFEQHALTEQMKELIYES 383  
 QY 360 IEMNPRIY 368  
 DB 384 IAFNPYQH 392

RESULT 12  
 AAB48047  
 ID AAB48047 standard; protein; 398 AA.  
 AC AAB48047;

XX  
 XX 19-MAR-2001 (first entry)  
 XX  
 XX Signal transduction protein.

XX Zea mays; maize; signal transduction protein; phytohormone; ethylene;  
 KW auxin; cytokinin; gibberellin; immunogen.  
 XX

OS Zea mays.

XX WO200070059-A2.

XX 23-NOV-2000.

XX 28-APR-2000; 2000WO-US011687.

XX 14-MAY-1999; 99US-0134292P.

XX 08-JUL-1999; 99US-0142996P.

XX (PION-) PIONEER HI-BRED INT INC.

XX Helentjaris TG;

XX

DR WPI; 2001-031929/04.  
 DR N-PSDB; AAC84262.  
 XX  
 PT New signal transduction nucleic acids and encoded proteins useful for  
 PT regulating phytohormone expression, including ethylene, auxins,  
 PT cytokinins and gibberellin, to provide control of plant response to  
 PT environmental stresses.  
 XX  
 PS Claim 13; Page 94; 126pp; English.

XX The invention provides Zea mays signal transduction proteins and encoding  
 CC nucleotide sequences. The nucleic acids are useful for regulating  
 CC expression of phytohormones, including ethylene, auxins, cytokinins, and  
 CC gibberellin, to effect developmental changes in plants and provide  
 CC control of plant response to environmental stresses. They may also be  
 CC used as probes or amplification primers in the detection, quantitation or  
 CC isolation of gene transcripts, for detecting mutations in the gene, for  
 CC monitoring upregulation of expression or changes in enzyme activity in  
 CC screening assays of compounds, for detection of any number of allelic  
 CC variants, or for site-directed mutagenesis in eukaryotic cells. They may  
 CC further be used for recombinant expression of their encoded polypeptides,  
 CC as immunogens in the preparation or screening of antibodies, and in sense  
 CC or antisense suppression of genes in a host cell, tissue or plant. The  
 CC proteins may be used in assays for enzyme agonists or antagonists, as  
 CC immunogens or antigens to obtain antibodies specifically immunoreactive  
 CC with the proteins. The present sequence represents a signal transduction  
 CC protein of the invention

XX Sequence 398 AA;

Query Match 72.9%; Score 1423; DB 4; Length 398;  
 Best Local Similarity 72.3%; Pred. No. 3.4e-137;  
 Matches 263; Conservative 50; Mismatches 49; Indels 2; Gaps 2;

QY 3 GAPVAEPTMTGGRVLLYDIFGNKPEVTNKYOPPIGPGAYGIVCSVMNPETREMV 62  
 DB 34 GVLMDNIQATLUSHGGRFIQYNIQNFIVETAKYKPPILPGKAYGIVCSALNSTAEQV 93  
 QY 63 AIKKIANAFNNDMDAKRTLREIKLRLHLDHENIIGIRDVIPPPIPOAFNDVYIATELMDT 122  
 DB 94 AIKKIANAFDNKIDAKRTLREIKLRLHMDHENIVAIRIIPPAQRAAFNDVYIATELMDT 153  
 QY 123 DLHHIIRSNQELSEHCQFYLIQILRGKYIHSANVIHRDLKPSNLLNANCDLKICD 182  
 DB 154 DLHQIIRSNQELSEHCQFYLIQILRGKYIHSANVLRDLKPSNLLNANCDLKICD 213  
 QY 183 LARPSSEDMTEYVTVTRWYRAPELLNSTDYSAA-DVWSVGCIFMELINRQPLPGRDH 241  
 DB 214 LARITSETDFMTEYVTVTRWYRAPELLNSTDYSAA-DVWSVGCIFMELINRQPLPGRDH 273  
 QY 242 MHQRLITEVIGTPTDDELGFIRNEDARKYMRHLPQYPRRTFASMPFRVOPAAALDLIERM 301  
 DB 274 VHQLRLMELIGTPEAEWEL-ENAKRYIQLPYRRQSFTKFPVHPTAIDLVEK 332  
 QY 302 LTFNPLORITVEALDHPYLERLHDADEPICLEPFSDFEQKALNEDQMKLIENEAIE 361  
 DB 333 LTFDPRRITVEGALAHPLASLHDSIDEPICMTFSDFEQHALSEQMKLIYQEAALA 392  
 QY 362 MNPN 365  
 DB 393 FNPD 396

RESULT 13  
 AAW15513  
 ID AAW15513 standard; protein; 423 AA.

XX AAW15513;

XX 04-JUN-1997 (first entry)

XX MAP kinase #2.

XX

KW Mitogen activated protein kinase; MAP; infectious specific protein;  
 KW plant; jasmonate acid.  
 OS Synthetic.  
 XX JP09065881-A.  
 PN 11-MAR-1997.  
 PD 29-AUG-1995; 95JP-00220935.  
 PF 29-AUG-1995; 95JP-00220935.  
 PR 29-AUG-1995; 95JP-00220935.  
 XX (NORQ ) NORINSUISANSO NOGO SEIBUTSU SHIGEN.  
 WP1; 1997-220416/20.  
 N-PSDB; AAT60350.  
 PT Wound-stress inducible MAP kinase - used to regulate the synthesis of  
 PT jasmonate acid.  
 XX Claim 3; Page 16-17; 21pp; Japanese.  
 PS AAW15512 and AAW15513 represent the mitogen activated protein (MAP)  
 CC kinases of the invention. This sequence contains the T-S-Y sequence, in  
 CC which the threonine and tyrosine residues are phosphorylated to activate  
 CC the protein at residues 249-251. The MAP kinase and its gene can be used  
 CC to regulate the synthesis of jasmonate acid and the synthesis of a group of  
 CC infectious specific proteins. By introducing the MAP kinase gene into a  
 CC plant, thereby inducing expression of the mRNA for MAP kinase (or its  
 CC antisense RNA), the synthesis of jasmonate acid and a group of infectious  
 CC specific proteins can be regulated in the plant  
 XX Sequence 423 AA;  
 SQ  
 Query Match 70.78; Score 1380.5; DB 2; Length 423;  
 Best Local Similarity 72.38; Pred. No. 8.8e-133;  
 Matches 253; Conservative 51; Mismatches 41; Indels 5; Gaps 3;  
 QY 16 GGRYLLYDIFGNKFEVNTKQPPIMPGRGAYGIVCSVMNFETREMAIKKIANAFNDM 75  
 DB 75 GGRFA-AAFGNPFETTKRPPIMPGRGAYGIVCSVLTNEMVAVKIANAFDIYM 133  
 QY 76 DAKRTREIKLRLHLDHENIIGIRDVTPPIPOAFNDVYIATLMDTDLHHIIRSNQELS 135  
 DB 134 DAKRTREIKLRLHLDHENIIGIRDVTPPIPOAFNDVYIATLMDTDLHHIIRSNQELS 190  
 QY 136 EHCQVFLYQILRGLKVIHSANVTHRDLPKSNLLNANCDLKICDFGLARPSSEDMNTE 195  
 DB 191 EDHCQVFLYQILRGLKVIHSANVTHRDLPKSNLLNANCDLKICDFGLARPSSEDMNTE 250  
 QY 196 YVTRWTRAPPELLINSTDYAA-DVMSVGCIFMELINRQPLFPGRDHQMLITEVIGT 254  
 DB 251 YVTRWTRAPPELLINSTDYAA-DVMSVGCIFMELINRQPLFPGRDHQMLITEVIGT 310  
 QY 255 PTDELGFIRNEDARKYRHLPOVPRTPFASMPFRVQPAALDLIERMLTNPQRIITVEE 314  
 DB 311 PTEADLGLQVEDAKRYIRLPQHPQELAEVPPHVNPLAIDLVDKMLTFDPTTRITVEE 370  
 QY 315 ALDHPYLERLHDIIDEICIEPSPDFEQALNEDQMKQLIFNEAIEWNP 364  
 DB 371 ALDHPYLERLHDIIDEICIEPSPDFEQALNEDQMKQLIFNEAIEWNP 420  
 RESULT 14  
 ADX79753  
 ID ADX79753 standard; protein; 318 AA.  
 XX  
 AC ADX79753;  
 XX  
 XX 21-APR-2005 (first entry)  
 XX Plant full length insert polypeptide seqid 49119.

XX plant protectant; plant growth regulant; gene therapy; plant;  
 KW recombinant DNA construct; physical array; plant breeding marker;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
 KW growth rate; cell cycle pathway; disease resistance;  
 KW galactomannan production; lignin production; plant growth regulator;  
 KW yield; plant growth; plant development; seed oil; protein yield;  
 XX protein content.  
 XX Unidentified.  
 XX US2004034888-A1.  
 XX 19-FEB-2004.  
 XX 28-APR-2003; 2003US-00425114.  
 PR 06-MAY-1999; 99US-00304517.  
 PR 05-NOV-2001; 2001US-00985678.  
 XX (LIUJ/) LIU J.  
 PA (ZHOU/) ZHOU Y.  
 PA (KOVA/) KOVALIC D K.  
 PA (SCRE/) SCREEN S E.  
 PA (TABAK/) TABASKA J E.  
 PA (CAOY/) CAO Y.  
 XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
 XX WPI; 2004-180133/17.  
 XX New recombinant DNA construct, useful for improving plant tolerance to  
 XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
 XX pests, for conferring increased resistance to plant disease, or for  
 XX improving yield.  
 XX Claim 1; SEQ ID NO 49119; 15pp; English.  
 XX The invention describes a recombinant DNA construct comprising a  
 XX polynucleotide consisting of a sequence encoding an amino acid sequence  
 XX available in electronic form from the US patent office at  
 XX ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide  
 XX of the invention are also useful in physical arrays of molecules and as  
 XX plant breeding markers. The recombinant DNA construct is useful for  
 XX improving plant tolerance to cold, heat, drought, herbicides, extreme  
 XX osmotic conditions, pathogens or pests, for manipulating growth rate in  
 XX plant cells by modification of the cell cycle pathway, for conferring  
 XX increased resistance to plant disease, for producing galactomannan,  
 XX lignin or plant growth regulators, for increasing the rate of homologous  
 XX recombination in plants, for improving yield by modification of  
 XX photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
 XX or by providing improved plant growth and development under at least one  
 XX stress condition or for modifying seed oil or protein yield and/or  
 XX content. This is the amino acid sequence of a plant full length insert  
 XX polypeptide that can be used in the recombinant DNA construct of the  
 XX invention.  
 XX Sequence 318 AA;  
 SQ  
 Query Match 68.6%; Score 1340.5; DB 8; Length 318;  
 Best Local Similarity 77.1%; Pred. No. 7.7e-129;  
 Matches 242; Conservative 46; Mismatches 25; Indels 1; Gaps 1;  
 QY 52 SVMNFETREMAIKKIANAFNDMDAKRTREIKLRLHLDHENIIGIRDVIPPPIPOAFN 111  
 DB 2 SLINTETNELVAVKIANAFNDMDAKRTREIKLRLHLDHENIIGIRDVIPPPIPOAFN 61  
 QY 112 DVYIATLMDTDLHHIIRSNQELSBEHCQVFLYQILRGLKVIHSANVTHRDLPKSNLLN 171  
 DB 62 DVYIATLMDTDLHHIIRSNQELSBEHCQVFLYQILRGLKVIHSANVTHRDLPKSNLLN 121  
 QY 172 ANCDLKICDFGLARPSSEDMNTEYVTRWTRAPPELLINSTDY-SAADVWSVGCIFMELI 230





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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1396	100.0	1396	15	AF479883 Oryza sat
2	1384.4	99.2	1396	15	AF216315 Oryza sat
3	1378.4	98.7	1457	15	OS250311 Oryza sat
4	1376.4	98.6	1411	15	AK104834 Oryza sat
5	1376.4	98.6	1490	15	AK067339 Oryza sat
6	1375.2	98.5	1424	15	AF332873 Oryza sat
7	1355	97.1	1356	15	OS4486975 Oryza sat
8	935.4	67.0	1113	15	AY738652 Saccharum
9	932.2	66.8	1452	15	AF079318 Triticum
10	925.2	66.3	1520	15	ASMAP1 X79993 A.sativa As
11	915.8	65.6	1125	6	AX048754 Sequence
12	808.4	57.9	1084	15	AF479884 Oryza sat
13	800.8	57.4	1647	15	AB016801 Zea mays
14	577.6	41.4	1464	15	AY642433 Brassica
15	558.8	40.0	1419	15	AY805424 Chorispot
16	543.4	38.9	1615	15	AK111942 Oryza sat
17	543.4	38.9	1678	15	AB183398 Oryza sat
18	543.4	38.9	1701	15	OS4553841 Oryza sat

19	538.2	38.6	1665	15	AF104247 Glycine m
20	532.4	38.1	1724	15	AK111691 Oryza sat
21	528.6	37.9	1643	15	AF153061 Pisum sat
22	523.8	37.5	1495	15	AF149424 Ipomoea b
23	514.2	36.8	1695	15	MSMMK4 X82270 M.sativa MM
24	514	36.8	1562	15	ATHATMPK6 D21842 Arabidopsis
25	514	36.8	1598	15	AV120737 Arabidops
26	513	36.7	1197	6	AX048762 Sequence
27	511.2	36.6	1197	6	AX048758 Sequence
28	508.8	36.4	1188	6	AX505949 Sequence
29	508.8	36.4	1188	6	AX505949 Sequence
30	504.8	36.2	2069	15	BT008855 Arabidops
31	504.2	36.1	1370	15	AB035141 Chlamydom
32	504.2	36.1	1480	15	D21839 Arabidopsis
33	504.2	36.1	1480	15	AF386961 Arabidops
34	503.8	36.1	1159	15	AY090981 Arabidops
35	497.8	35.7	1212	15	BT000007 Arabidops
36	495.8	35.5	1644	15	AY173962 Triticum
37	494.6	35.4	1506	15	AF247135 Capsicum
38	494.4	35.4	1195	15	DQ078119 Rheum aus
39	493	35.3	1522	15	AB098729 Nicotiana
40	492.2	35.3	1186	15	X70703 P.sativum m
41	491.8	35.2	1632	15	AF329506 Glycine m
42	489.2	35.0	1122	15	AB016802 Zea mays
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## ALIGNMENTS

### RESULT 1

AF479883

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBLISHED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBLISHED

REFERENCE

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JOURNAL

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REFERENCE

AUTHORS

TITLE

JOURNAL

PUBLISHED

REFERENCE

AUTHORS

TITLE

JOURNAL

AF479883 Oryza sativa MAP kinase MAPK5a (MAPK5) mRNA, complete cds, alternatively spliced.

AF479883

AF479883.1 GI:19401851

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzoideae; Oryza.

Xiong, L. and Yang, Y.

1 (bases 1 to 1396)

Disease Resistance and Abiotic Stress Tolerance in Rice Are

Inversely Modulated by an Abscissic Acid-Inducible Mitogen-Activated

Protein Kinase

Plant Cell 15 (3), 745-759 (2003)

12615946

Xiong, L., Qi, M. and Yang, Y.

Molecular cloning and characterization of a novel MAP kinase,

OSMAPK5, in rice

Unpublished

3 (bases 1 to 1396)

Xiong, L., Qi, M. and Yang, Y.

Direct Submission

Submitted (01-FEB-2002) Plant Pathology, University of Arkansas,

217 Plant Science Building, Fayetteville, AR 72701, USA

Location/Qualifiers

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 5.6e-185;
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DB 1381 AAAAAAAAAAAAAAAAAA 1396

RESULT 2
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DEFINITION Oryza sativa MAP kinase 1 mRNA, complete cds.
ACCESSION AF216315
VERSION AF216315.1 GI:11869990
KEYWORDS Oryza sativa
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 1396)
AUTHORS Wen, J. Q., Oono, K. and Imai, R.
TITLE Two Novel Mitogen-Activated Protein Signaling Components, OsMEK1
and OsMAP1, Are Involved in a Moderate Low-Temperature Signaling
Pathway in Rice
JOURNAL Plant Physiol. 129 (4), 1880-1891 (2002).
PUBMED 12177502
REFERENCE 2 (bases 1 to 1396)
AUTHORS Wen, J. Q. and Imai, R.
TITLE Direct Submission
JOURNAL Submitted (15-DEC-1999) Department of Low Temperature Sciences,
Hokkaido National Agricultural Experiment Station, Hitsujigaoka-1,
Toyohira-ku, Sapporo, Hokkaido 062-8555, Japan
FEATURES
Location/Qualifiers
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## ORIGIN

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Best Local Similarity 99.9%; Pred. No. 2.3e-183;
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QY  61 AGAGAGGAGGATAGGATGAGCGCGCGCGCGGTCGCGGAGTTCCAGGCCGACGATGACGC 120
DB  71 AGAGAGGAGGATAGGATGAGCGCGCGCGCGGTCGCGGAGTTCCAGGCCGACGATGACGC 130
QY  121 ACGCCCGCGGTAACCTCTCTACGACATCTTCGGGAAACAAAGTTCGAGGTGACGAAACAAAGT 180
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QY  181 ACCNAGCGCCCATCATGCCCATTCGGCGCGCGCGCTACGGGATCGTCTCGTGGATGA 240
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DB  1391 AAAAAA 1396

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ACCESSION     AJ250311
VERSION       AJ250311.1 GI:10862875
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SOURCE         Oryza sativa
ORGANISM      Oryza sativa
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               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE     1 Huang,H.J., Dai,Y.H., Huang,D.D. and Kuo,T.T.
               Molecular Cloning of a Low Temperature-Inducible MAP Kinase from
               Rice
JOURNAL       Unpublished
REFERENCE     2 (bases 1 to 1457)
AUTHORS       Huang,H.J.
TITLE         Direct Submission
JOURNAL       Submitted (15-OCT-1999) Huang H.J., Department of Biology,
               Cheng-Kung University, 1, University Rd., Tainan 701, TAIWAN
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Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN, Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M. and Hayashizaki, Y.  
Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice  
Science 301 (5631), 376-379 (2003)  
12869764

## TITLE

## JOURNAL

## PUBMED

## REFERENCE

## AUTHORS

2 (bases 1 to 1411)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, Y., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Osato, N., Ota, Y., Otomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, P., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.  
Direct Submission

## TITLE

## JOURNAL

Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail: skikuchi@nias.affrc.go.jp, Tel: 81-29-838-7007, Fax: 81-29-838-7007)  
This clone is one of the 28K full-length cDNA clones from japonica rice.  
URL: <http://cdna01.dna.affrc.go.jp/cDNA/>

## COMMENT

NIAS Rice Full-Length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and Yamamoto, M.

PAIS Genome Sequencing & Analysis Group: Otono, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K.  
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, P., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.  
Location/Qualifiers

## FEATURES

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## ORIGIN

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DEFINITION Oryza sativa MAP kinase BIMK1 mRNA, complete cds.
ACCESSION AF332873
VERSION AF332873.1 GI:12698875
KEYWORDS Oryza sativa (indica cultivar-group)
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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REFERENCE 1 (bases 1 to 1424)
AUTHORS Song, F. and Goodman, R.M.
TITLE OsBIMK1, a novel MAP kinase from rice that is involved in systemic
acquired resistance
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1424)
AUTHORS Song, F. and Goodman, R.M.
TITLE Direct Submission
JOURNAL Submitted (30-DEC-2000) Department of Plant Pathology, University
of Wisconsin-Madison, 1630 Linden Drive, Madison, WI 53706, USA
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LOCUS AF079318
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ACCESSION AF079318
VERSION AF079318.1 GI:3396051
KEYWORDS .
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ORGANISM Triticum aestivum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 1452)
Takezawa, D.
Biotector- and A23187-induced expression of WCK-1, a gene encoding
mitogen-activated protein kinase in wheat
Plant Mol. Biol. 40 (6), 921-933 (1999)
REFERENCE 2 (bases 1 to 1452)
Takezawa, D.
Direct Submission
Submitted (21-JUL-1998) Basic Cryoscience, Institute of Low
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 ORGANISM Avena sativa  
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 1  
 Huttly,A.K. and Phillips,A.L.  
 Gibberellin-regulated expression in oat aleurone cells of two  
 kinases that show homology to MAP kinase and a ribosomal protein  
 kinase  
 JOURNAL Plant Mol. Biol. 27 (5), 1043-1052 (1995)  
 PUBMED 7766874

# REFERENCE

AUTHORS Huttly,A.K.  
 TITLE Direct Submission  
 JOURNAL Submitted (30-JUN-1994) A.K. Huttly, Institute of Arable Crops Research, Univ. of Bristol, Dept of Agricultural Sciences, Long Ashton Research Station, Bristol, BS18 9AF, UK

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clade; Panicoideae; Andropogoneae; Zea.
1
REFERENCE 1
AUTHORS Helentjaris, T.G.
TITLE Signal transduction genes and methods of use
JOURNAL Patent: WO 0070059-A 25 23-NOV-2000; (US)
PIONEER HI-BRED INTERNATIONAL, INC. (US)
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Best Local Similarity 88.7%; Pred. No. 4.3e-118;
Matches 992; Conservative 0; Mismatches 127; Indels 0; Gaps 0;
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**AUTHORS**  
**TITLE**  
**JOURNAL**  
**PUBMED**  
**REFERENCE**  
**AUTHORS**  
**TITLE**  
**JOURNAL**

Berberich, T., Sano, H. and Kusano, T.  
 Involvement of a MAP kinase, ZmMPK5, in senescence and recovery  
 from low-temperature stress in maize  
 Mol. Gen. Genet. 262 (3), 534-542 (1999)  
 10589842  
 2 (bases 1 to 1647)  
 Kusano, T.  
 Direct Submission  
 Submitted (07-AUG-1998) Tomonobu Kusano, Nara Institute of Science  
 and Technology, Research and Education Center for Genetic  
 Information, 8916-5 Takayama-cho, Ikoma, Nara 630-0101, Japan  
 (E-mail: kusano@nara.ac.jp, Tel: 81-743-72-5651,  
 Fax: 81-743-72-5659)

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CDS

ORIGIN

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 ACCESSION  
 AY642433  
 VERSION  
 AY642433.1  
 GI:54402039  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Brassica napus (rape)  
 Brassica napus  
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 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 REFERENCE  
 1 (bases 1 to 1464)  
 Yu, S., Zhang, L., Zuo, K., Tang, D. and Tang, K.  
 Isolation and characterization of an oilseed rape MAP kinase BnMPK3  
 involved in diverse environmental stresses  
 Plant Sci. 169 (2), 413-421 (2005)  
 JOURNAL  
 REFERENCE  
 2 (bases 1 to 1464)  
 Yu, S., Zhang, L., Zuo, K., Tang, D. and Tang, K.  
 Direct Submission  
 Submitted (01-JUN-2004) Agriculture and Biology, Plant

Biotechnology Research Center, 1954# Huashan Road, Shanghai 200030,  
China

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## RESULT 15

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LOCUS

Chorisporea bungeana 1419 bp mRNA linear PLN 28-NOV-2004  
complete cds.

ACCESSION

AY805424

VERSION

AY805424.1

KEYWORDS

SOURCE

ORGANISM

Chorisporea bungeana

Chorisporea bungeana

Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eutrosids II; Brassicales; Brassicaceae; Chorispora.

REFERENCE

1 (bases 1 to 1419)

Zhang, T., An, L., Wang, J., Si, J., and Zhang, H.

Direct Submission

Submitted (01-NOV-2004) School of Life Science, Lanzhou University,

Tianshui South Road 222, Lanzhou, Gansu 730000, P.R.China

Location/Qualifiers

FEATURES

source

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40.0%; Score 558.8; DB 15; Length 1419;

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